

Result No.	Score	Query			DB	ID	Description
		Match	Length	No.			
1	17	94.4	794	1	AJ641058	AJ641058 AJ641058	
C 2	16	88.9	312	2	BE153987	BE153987 PMO-HT033	
	3	16	88.9	340	3	BI432519	BI432519 EST535280
C 4	16	88.9	439	8	TI14826	TI14826 crs268 lamb	
C 5	16	88.9	500	3	BP191036	BP191036 BP191036	
C 6	16	88.9	652	2	BG600462	BG600462 EST505357	
C 7	16	88.9	740	8	CX409188	CX409188 JGI_X2T32	
C 8	16	88.9	747	10	CL169941	CL169941 104_370	
C 9	16	88.9	752	10	CW385375	CW385375 fsb501f	
C 10	16	88.9	759	2	BG899203	BG899203 EST515054	
C 11	16	88.9	761	10	CL169940	CL169940 104_370	
C 12	16	88.9	1030	10	CL033121	CL033121 CHA16-3f6	
C 13	15	83.3	85	6	CD963839	CD963839 SDY_133 G	
C 14	15	83.3	95	10	CG560188	CG560188 OST18026	
C 15	15	83.3	102	10	CG671007	CG671007 OST47216	
C 16	15	83.3	208	7	CO323095	CO323095 BK189652	
C 17	15	83.3	238	10	CG556891	CG556891 OST17287	
C 18	15	83.3	247	8	CX626914	CX626914 GAN008N05	
C 19	15	83.3	285	3	BI491822	BI491822 df15e12.w	
C 20	15	83.3	306	2	BF333376	BF333376 QV1-HT063	
C 21	15	83.3	308	2	BG184004	BG184004 RST2919 A	
C 22	15	83.3	336	2	BG790049	BG790049 sae62d11.A	

```

DEFINITION PMO-HT0339-060400-009-C04 HT0339 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE153987
VERSION BE153987.1 GI:8616617
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE 1 (bases 1 to 312)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=4&t2=PMO-HT0339-060400-009-C04&t3=2000-04-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 226.
Location/Qualifiers
1..312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0339"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 312;
Best Local Similarity 68.8%; Pred. No. 1e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUAGGCCGCGC 16
|:|:|:|:|:|:|:|:|:|
Db 289 ATATTATGCGCTGCTC 274

RESULT 3
BI432519/c 340 bp mRNA linear EST 30-APR-2003
LOCUS EST535280 P. infestans-challenged potato leaf, compatible reaction
DEFINITION Solanum tuberosum cDNA clone PPCAR82 5' sequence, mRNA sequence.
ACCESSION BI432519
VERSION BI432519.1 GI:15257209
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiales; Solanales; Solanaceae; Solanum.

Query Match 88.9%; Score 16; DB 2; Length 312;
Best Local Similarity 68.8%; Pred. No. 1e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUAGGCCGCGC 16
|:|:|:|:|:|:|:|:|:|
Db 289 ATATTATGCGCTGCTC 274

RESULT 3
BI432519/c 340 bp mRNA linear EST 30-APR-2003
LOCUS EST535280 P. infestans-challenged potato leaf, compatible reaction
DEFINITION Solanum tuberosum cDNA clone PPCAR82 5' sequence, mRNA sequence.
ACCESSION BI432519
VERSION BI432519.1 GI:15257209
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiales; Solanales; Solanaceae; Solanum.

```

```

REFERENCE 1 (bases 1 to 340)
AUTHORS Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
Bougril,O., Buelli,C.R., Roming,C.M., Fry,W.E. and Baker,B.
TITLE Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible Interaction
JOURNAL Unpublished (2000)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
Location/Qualifiers
1..340
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCAR82"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf,
compatible reaction"
/note="vector: pluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Cornell University, Fry lab; sequencing:
The Institute for Genomic Research; Whole plants were
challenged with 20,000 sporangia/ml of the compatible P.
infestans isolate US 940480. Leaf tissue was collected at
3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
in liquid nitrogen immediately upon removal. Kennebec
plants showed first symptoms of infection at 48 hours
after inoculation. NOTE: We cannot exclude the
possibility that this sequence is actually derived from
Phytophthora rather than potato."
ORIGIN
Query Match 88.9%; Score 16; DB 3; Length 340;
Best Local Similarity 68.8%; Pred. No. 1e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUAUAGGCCGCGCUC 18
|:|:|:|:|:|:|:|:|:|
Db 283 AATTATGCGCTGCTC 268

RESULT 4
TI4826/c 439 bp mRNA linear EST 28-JUL-1995
LOCUS crs268 lambdaZAPST Ricinus communis cDNA clone pcrs268, mRNA
DEFINITION sequence.
ACCESSION TI4826
VERSION TI4826.1 GI:688463
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Malpighiales; Euphorbiales; Acalyphoideae;
            Acalyphaeae; Ricinus.
REFERENCE 1 (bases 1 to 439)
AUTHORS vandelaar,F.J., Turner,S. and Somerville,C.
TITLE Expressed sequence tags from developing castor seeds
JOURNAL Plant Physiol. 108, 1141-1150 (1995)
COMMENT Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CA 94305
Tel: 415251521
Email: crs@andrew.stanford.edu
Seq primer: T3.
Location/Qualifiers

```

```

source
1. .439
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone_lib="lambdaZAPST"
/notes="Vector: lambdaZAPII; Site 1: EcoRI; Site 2: XhoI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPII according
to the instructions of the manufacturer (Stratagene):
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN
Query Match      88.9%; Score 16; DB 8; Length 439;
Best Local Similarity 68.8%; Pred. No. 1e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUGGCCCGCUC 18
||:::||:::||::||
Db 332 AATTATGGCCCTGCTC 317

RESULT 5
BP191026 500 bp mRNA linear EST 17-JUL-2003
LOCUS BP191026 planarian head cDNA Dugesia japonica cDNA clone 06171_HH,
DEFINITION mRNA sequence.
ACCESSION BP191026
VERSION BP191026.1 GI:32905550
KEYWORDS EST.
SOURCE Dugesia japonica
ORGANISM Dugesia japonica
Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata;
Tricladida; Paludicola; Dugesidae; Dugesia.
1 (bases 1 to 500)
Mineta,K., Nakazawa,M., Cebria,F., Ikeo,K., Agata,K. and
Gojobori,T.
Origin and evolutionary process of the CNS elucidated by
comparative genomics analysis of planarian ESTs
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7666-7671 (2003)
12802012
Contact: Katsuhiko Mineta
National Institute of Genetics, Center for Information Biology and
DNA Data Bank of Japan
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6847
Fax: 81-559-81-6848
Email: kmineta@lab.nig.ac.jp
These clones and additional information are obtained from our web
site: http://www.cib.nig.ac.jp/dda/.

FEATURES
Location/Qualifiers
1. .500
/organism="Dugesia japonica"
/mol_type="mRNA"
/db_xref="taxon:6161"
/clone="06171_HH"
/tissue_type="head"
/dev_stage="adult"
/clone_lib="planarian head cDNA"

ORIGIN
Query Match      88.9%; Score 16; DB 3; Length 500;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAAUUAUGGCCCGCUC 17
||:::||:::||::||

source
1. .439
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone_lib="lambdaZAPST"
/notes="Vector: lambdaZAPII; Site 1: EcoRI; Site 2: XhoI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPII according
to the instructions of the manufacturer (Stratagene):
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN
Query Match      88.9%; Score 16; DB 8; Length 439;
Best Local Similarity 68.8%; Pred. No. 1e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUGGCCCGCUC 18
||:::||:::||::||
Db 332 AATTATGGCCCTGCTC 317

RESULT 6
BG600462 652 bp mRNA linear EST 07-MAR-2003
LOCUS BG600462 cSTS Solanum tuberosum cDNA clone CSTS2911 5' sequence,
DEFINITION mRNA sequence.
ACCESSION BG600462
VERSION BG600462.1 GI:13617598
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 652)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Roming,C., Tanksley,S. and Baker,B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.

FEATURES
Location/Qualifiers
1. .652
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="CSTS2911"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone_lib="cSTS"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 652;
Best Local Similarity 68.8%; Pred. No. 1.1e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUGGCCCGCUC 18
||:::||:::||::||
Db 536 AATTATGGCCCTGCTC 521

RESULT 7
CX409188 740 bp mRNA linear EST 06-JAN-2005
LOCUS CX409188 JGI_XZT32096.fwd NIH_XGC tropTad5 Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7608418 5', mRNA sequence.
ACCESSION CX409188
VERSION CX409188.1 GI:57189890
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 740)
Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.

```





/mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone="f6bb001f069k13"  
 /clone\_lib="Sorghum methylation filtered library (LibID: 104)"

/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

## ORIGIN

Query Match 88.9%; Score 16; DB 10; Length 752;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAUAUAGGCCCGUCU 17

Db 614 TAATTATGGCCTGCT 599

RESULT 10  
BG889203/c

LOCUS  
 DEFINITION EST515054 cSTD Solanum tuberosum cDNA clone cSTD13G2 5' sequence, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Solanum tuberosum (potato)  
 Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE

AUTHORS

van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chiemingo, A., Bougri, O., Buell, C. R., Renning, C., Tanksley, S. and Baker, B.

TITLE

JOURNAL

COMMENT

The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:  
 http://genome.arizona.edu/orders/  
 Seq primer: M13P-R.

## FEATURES

source

1..759  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="cSTD13G2"  
 /tissue\_type="dormant tuber"  
 /dev\_stage="one month post-harvest"  
 /lab\_host="SOLR"  
 /clone\_lib="cSTD"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."

## ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 759;  
 Best Local Similarity 68.8%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUAUAGGCCCGUCUC 18

Db 621 AATTATGGCCTGCTC 606

RESULT 11

CL169940/c

LOCUS

DEFINITION

CL169940 761 bp DNA linear GSS 06-JAN-2004  
 104 370 10813405 116 31789 109 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

AUTHORS

Bedell, J. A., Budiman, M. A., Nunberg, A., Citek, R. W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B. A., Wilsey, G., Korff, I. F., Rabinowicz, P. D., Lakey, N., McCombie, W. R., Jeddeloh, J. A. and Martienssen, R. A.

TITLE

JOURNAL

PUBMED

COMMENT

Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
 15660154  
 Contact: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@origenomics.com  
 Plate: 370 row: e column: 13  
 Seq primer: T3 Reverse  
 Class: methylation filtered  
 High quality sequence stop: 761.

## FEATURES

source

1..761  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone="10813405"  
 /clone\_lib="Sorghum methylation-filtered library (LibID: 104)"

/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."

## ORIGIN

Query Match 88.9%; Score 16; DB 10; Length 761;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAUAUAGGCCCGUCU 17

Db 654 TAATTATGGCCTGCT 639

RESULT 12

CL033121

LOCUS

DEFINITION

CL033121 1030 bp DNA linear GSS 31-DEC-2003  
 CH216-36A12 Sp6.1 CH216 Xenopus tropicalis genomic clone

ACCESSION

VERSION

KEYWORDS

CH216-36A12, genomic survey sequence.  
 CL033121  
 GSS.



ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 102)  
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
Sparks,M.J., Van Slijkenhorst,I., Vogel,P., Walke,W., Xu,N.,  
Zhu,Q., Person,C. and Sands,A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED 14610273

COMMENT Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

FEATURES  
source Location/Qualifiers  
1..102  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST472166"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

ORIGIN  
Query Match 83.3%; Score 15; DB 10; Length 102;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 UAAUUAUGGCCUGC 16  
:|:|:|:|:|:|  
Db 42 TAATTATGGCCCTGC 28

Search completed: November 30, 2005, 00:44:45  
Job time : 1867.5 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:31 ; Search time 136.5 Seconds  
(without alignments)  
19.597 Million cell updates/sec

Title: US-10-018-716B-2

Perfect score: 18

Sequence: 1 auaauuagggccugcuc 18

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 3205263 seqs, 74304013 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA\_New.\*  
1: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
2: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
5: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
7: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
8: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
9: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq3:\*  
10: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	77.8	1149	9	US-11-082-389-213
2	12	66.7	19	8	US-11-101-244-173294
3	12	66.7	19	8	US-11-101-244-339765
4	12	66.7	19	8	US-11-101-244-600029
5	12	66.7	19	8	US-11-101-244-1044082
6	12	66.7	19	8	US-11-101-244-1044118
7	12	66.7	19	8	US-11-101-244-1152178
8	12	66.7	19	8	US-11-101-244-1152276
9	12	66.7	19	8	US-11-101-244-1311535
10	12	66.7	19	8	US-11-101-244-1430673
11	12	66.7	19	8	US-11-101-244-1430674
12	12	66.7	19	9	US-11-083-784-173294
13	12	66.7	19	9	US-11-083-784-339765
14	12	66.7	19	9	US-11-083-784-600029
15	12	66.7	19	9	US-11-083-784-1044082
16	12	66.7	19	9	US-11-083-784-1044118
17	12	66.7	19	9	US-11-083-784-1152178
18	12	66.7	19	9	US-11-083-784-1152276
19	12	66.7	19	9	US-11-083-784-1311535
20	12	66.7	19	9	US-11-083-784-1430673
21	12	66.7	19	9	US-11-083-784-1430674
22	12	66.7	844	9	US-11-082-389-441
23	12	66.7	1095	9	US-11-082-389-439

Sequence 239, App  
Sequence 3510, App  
Sequence 164, App  
Sequence 1, Appli  
Sequence 341877,  
Sequence 343613,  
Sequence 343631,  
Sequence 374101,  
Sequence 380293,  
Sequence 425500,  
Sequence 425510,  
Sequence 425572,  
Sequence 661639,  
Sequence 661697,  
Sequence 716963,  
Sequence 716974,  
Sequence 725866,  
Sequence 764763,  
Sequence 764784,  
Sequence 764830,  
Sequence 799257,  
Sequence 828288,

24 12 66.7 1656 1 US-10-131-826A-239  
25 12 66.7 3458 1 US-10-793-626-3510  
26 12 66.7 6708 1 US-10-821-234-164  
27 12 66.7 7382 1 US-10-839-211-1  
28 11 61.1 19 8 US-11-101-244-341877  
29 11 61.1 19 8 US-11-101-244-343613  
30 11 61.1 19 8 US-11-101-244-343631  
31 11 61.1 19 8 US-11-101-244-374101  
32 11 61.1 19 8 US-11-101-244-380293  
33 11 61.1 19 8 US-11-101-244-425500  
34 11 61.1 19 8 US-11-101-244-425510  
35 11 61.1 19 8 US-11-101-244-425572  
36 11 61.1 19 8 US-11-101-244-661639  
37 11 61.1 19 8 US-11-101-244-661697  
38 11 61.1 19 8 US-11-101-244-716963  
39 11 61.1 19 8 US-11-101-244-716974  
40 11 61.1 19 8 US-11-101-244-725866  
41 11 61.1 19 8 US-11-101-244-764763  
42 11 61.1 19 8 US-11-101-244-764784  
43 11 61.1 19 8 US-11-101-244-764830  
44 11 61.1 19 8 US-11-101-244-799257  
45 11 61.1 19 8 US-11-101-244-828288

ALIGNMENTS

RESULT 1

US-11-082-389-213  
; Sequence 213, Application US/11082389  
; Publication No. US2005024935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Habernauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; FILE REFERENCE: BGI-131CPCN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 213  
; LENGTH: 1149  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1126)  
; OTHER INFORMATION: RXN00523

US-11-082-389-213

Query Match 77.8%; Score 14; DB 9; Length 1149;  
Best Local Similarity 64.3%; Pred.No. 2.3;  
Matches 9; Conservative 5; Mismatches 0; Indels

Qy 5 UUAUGGCCCGUC 18  
:::|||||:  
Db 229 TTATGGCCCTGCTC 24

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RESULT 2
US-11-101-244-173294
; Sequence 173294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1134499US

```

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels

Qy 6 UAUGGCCUGCU 17  
|||  
Db 3 UAUGGCCUGCU 14

```

RESULT 3
US-11-101-244-339765/c
; Sequence 339765, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 11498US

```

Query Match	66.7%	Score 12;	DB 8;	Length 19;
Best Local Similarity	66.7%	Pred. No. 34;		
Matches 8;	Conservative 4;	Mismatches 0;	Indels	

Qy 2 UAAUUAUGGCC 13  
:|:|:|:|:|  
Db 19 TAAATTATGGCC 8

RESULT 4  
US-11-101-244-600029  
; Sequence 600029, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: J3499US  
; CURRENT APPLICATION NUMBER: US/11/101.244

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels

Qy 7 AUGGCCUGCUC 18  
|||||  
pb 3 AUGGCCUGCUC 14

```

RESULT 5
US-11-101-244-1044082
; Sequence 1044082, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13490US

```

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCUGCUC 18  
|||||  
DB 3 AUGGCCUGCUC 14

## RESULT 6

US-11-101-244-1044118  
; Sequence 1044118, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1044118  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1044118

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCUGCUC 18  
|||||  
DB 5 AUGGCCUGCUC 16

## RESULT 7

US-11-101-244-1152178  
; Sequence 1152178, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1152178  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1152178

Query Match 66.7%; Score 12; DB 8; Length 19;

Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCUGCUC 18  
|||||  
DB 5 AUGGCCUGCUC 16

## RESULT 8

US-11-101-244-1152276  
; Sequence 1152276, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1152276  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1152276

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCUGCUC 18  
|||||  
DB 5 AUGGCCUGCUC 16

## RESULT 9

US-11-101-244-1311535  
; Sequence 1311535, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1311535  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1311535

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUUUAUGGCC 12  
|:|||||:|:  
Db 3 AUAUUUAUGGCC 14

RESULT 10  
US-11-101-244-1430673/c  
; Sequence 1430673, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1430673  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1430673

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCCGUCU 18  
|:|||||:|:  
Db 12 ATGGCCCTGCTC 1

RESULT 11  
US-11-101-244-1430674/c  
; Sequence 1430674, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1430674  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1430674

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCCGUCU 18  
|:|||||:|:  
Db 15 ATGGCCCTGCTC 4

RESULT 12  
US-11-083-784-173294  
; Sequence 173294, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 173294  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-173294

Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 UAUGGCCCGUCU 17  
|:|||||:|:  
Db 3 UAUGGCCCGUCU 14

RESULT 13  
US-11-083-784-339765/c  
; Sequence 339765, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 339765  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-339765



Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 66.7%; Pred. No. 34;  
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAAUUAUGGCC 13  
Db 19 TAAATATGGCCC 8

RESULT 14

US-11-083-784-600029  
; Sequence 600029, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 600029  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-600029

Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCCGCUC 18  
Db 3 AUGGCCCGCUC 14

RESULT 15

US-11-083-784-1044082  
; Sequence 1044082, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1044082  
; LENGTH: 19  
; TYPE: RNA

; ORGANISM: Homo sapiens  
US-11-083-784-1044082

Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AUGGCCCGCUC 18  
Db 3 AUGGCCCGCUC 14

Search completed: November 29, 2005, 18:29:39  
Job time : 136.5 secs

***This Page Blank (usp10)***

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:31 ; Search time 72 Seconds  
(without alignments)  
444.390 Million cell updates/sec

Title: US-10-018-716B-2

Perfect score: 18

Sequence: 1 aaauuauagccugcuc 18

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/PCUS COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfilese1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	2179	2	US-08-487-886-1
2	18	100.0	2179	2	US-08-531-070A-1
3	18	100.0	2179	3	US-08-482-855-1
4	18	100.0	2179	3	US-08-474-986-1
5	18	100.0	2393	3	US-09-016-434-1209
6	15	83.3	481	3	US-09-270-767-1666
7	15	83.3	481	3	US-09-270-767-16948
8	15	83.3	52992	3	US-09-949-016-16105
9	14	77.8	900	3	US-09-489-039A-6986
10	14	77.8	1149	3	US-09-602-787A-379
11	14	77.8	1887	3	US-09-620-312D-42
12	14	77.8	3678	3	US-09-112-580-13
13	14	77.8	3762	3	US-09-489-039A-4926
14	14	77.8	55264	3	US-09-949-016-15014
15	14	77.8	70828	3	US-09-949-016-12122
16	14	77.8	94755	3	US-09-949-016-11839
17	14	77.8	101951	3	US-09-949-016-15648
18	14	77.8	137226	3	US-09-949-016-13763
19	14	77.8	139936	3	US-09-949-016-11782
20	14	77.8	139952	3	US-09-949-016-13280
21	14	77.8	147840	3	US-09-949-016-15236
22	13	72.2	25	3	US-09-396-196G-44948
23	13	72.2	339	3	US-09-489-039A-6054
24	13	72.2	459	3	US-09-248-796A-1604

25	13	72.2	601	3	US-09-949-016-48726	Sequence 48726, A
26	13	72.2	601	3	US-09-949-016-156620	Sequence 156620, A
27	13	72.2	601	3	US-09-949-016-160355	Sequence 160355, A
28	13	72.2	601	3	US-09-949-016-160356	Sequence 160356, A
29	13	72.2	668	3	US-09-533-559-5223	Sequence 5223, Ap
30	13	72.2	886	2	US-08-469-427A-1	Sequence 1, Appli
31	13	72.2	886	2	US-08-609-443B-1	Sequence 1, Appli
32	13	72.2	886	2	US-08-569-063C-1	Sequence 1, Appli
33	13	72.2	886	2	US-08-851-896-1	Sequence 1, Appli
34	13	72.2	1443	3	US-09-489-039A-5874	Sequence 5874, Ap
35	13	72.2	2554	3	US-09-701-868-4	Sequence 4, Appli
36	13	72.2	7883	3	US-09-949-016-11183	Sequence 13183, A
37	13	72.2	8773	3	US-09-949-016-14496	Sequence 14496, A
38	13	72.2	9792	3	US-09-635-872A-14	Sequence 14, Appl
39	13	72.2	9792	3	US-09-636-077A-14	Sequence 14, Appl
40	13	72.2	9792	3	US-09-636-060C-14	Sequence 14, Appl
41	13	72.2	9792	3	US-09-986-552-14	Sequence 14, Appl
42	13	72.2	9792	3	US-09-636-596C-14	Sequence 21, Appl
43	13	72.2	9792	3	US-10-023-894-21	Sequence 14, Appl
44	13	72.2	9792	3	US-10-306-686-14	Sequence 14, Appl
45	13	72.2	9792	3	US-09-895-072-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-08-487-886-1  
; Sequence 1, Application US/08487886  
; Patent No. 5744448  
; GENERAL INFORMATION:  
; APPLICANT: Kelton, Christie Ann  
; APPLICANT: Schweickhardt, Rene Lynn  
; APPLICANT: Cheng, Shirley Vui Yen  
; APPLICANT: Nugent, No. 5744448een Patrice  
; TITLE OF INVENTION: Human Follicle Stimulating  
; TITLE OF INVENTION: Hormone Receptor  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stephan P. Williams,  
; ADDRESSEE: Ares-Serono, Inc.  
; STREET: Exchange Place, 37th floor  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
; COMPUTER: IBM PS/2, model 55 SX  
; OPERATING SYSTEM: MS-DOS version 4.0  
; SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,886  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/670,085  
; FILING DATE: 15-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Stephan P.  
; REGISTRATION NUMBER: 28546  
; REFERENCE/DOCKET NUMBER: US/252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 723-1300  
; TELEFAX: (617) 723-8923  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2179  
; TYPE: Nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; MOLECULE TYPE: cdna to mRNA  
; ORIGINAL SOURCE:

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: ORGANISM: Homo sapiens
:
: TISSUE TYPE: Testis
:
: IMMEDIATE SOURCE:
:
: LIBRARY: 19111 cDNA library, Clontech #HL1010b
:
: CLONE: pFHSR11-11, pFHSR15-6
:
: FEATURE:
:
: NAME/KEY: protein coding region
:
: LOCATION: 75 to 2159
:
: US-08-487-886-1

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Query Match 100.0%; Score 18; DB 2; Length 2179;  
Best Local Similarity 66.7%; Pred.No. 0.21;  
Matches 12; Conservative 6; Mismatches 0; Indels

QY 1 AUAUUAUGGCCCGUC 18  
|:|:|:|:|:|:|:|:  
Db 69 ATAATTATGGCCCTGCTC 86

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RESULT 2
US-08-531-070A-1
; Sequence 1, Application US/08531070A
; Patent No. 5851768
; GENERAL INFORMATION:
; APPLICANT: de la Chapelle, Albert
; APPLICANT: Aittomaki, Kristiina
; APPLICANT: Huhtaniemi, Ilpo
; TITLE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesis
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

```

COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/531,070A  
FILING DATE: 20-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gags, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28113/32879  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEO ID NO: 1:

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SEQUENCE CHARACTERISTICS:
  LENGTH: 2179 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  -08-531-070A-1

Query Match      100.0%; Score 18; DB 2; Length 2179;
Best Local Similarity 66.7%; Pred. No. 0.21;
Matches 12; Conservative 6; Mismatches 0; Indels

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Qy 1 AUAUUAUGGCCUGCUC 18  
|:|:|:|:|:|:|:|:  
Db 69 ATAATTATGGCCCTGCTC 86

RESULT 3  
US-08-482-855-1

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1 Sequence 1, Application US/08482855
2 Patent No. 6121016
3 GENERAL INFORMATION:
4 APPLICANT: Kelton, Christie Ann
5 APPLICANT: Schweickhardt, Rene Lynn
6 APPLICANT: Cheng, Shirley Vui Yen
7 APPLICANT: Nugent, No. 6121016een Patrice
8 TITLE OF INVENTION: Human Follicle Stimulating
9 TITLE OF INVENTION: Hormone Receptor
10 NUMBER OF SEQUENCES: 2
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Stephan P. Williams,
13 ADDRESSEE: Ares-Serono, Inc.
14 STREET: Exchange place, 37th floor
15 CITY: Boston
16 STATE: MA
17 COUNTRY: USA
18 ZIP: 02109
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
21 COMPUTER: IBM PS/2, model 55 SX
22 OPERATING SYSTEM: MS-DOS version 4.0
23 SOFTWARE: VAX/VMS Massbl via Kermit to IBM MS-DOS
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/482,855
26 FILING DATE: 07-JUN-1995
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 07/670,085
30 FILING DATE: 15-MAR-1991
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Williams, Stephan P.
33 REGISTRATION NUMBER: 28546
34 REFERENCE/DOCKET NUMBER: US/252
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (617) 723-1300
37 TELEFAX: (617) 723-8923
38 INFORMATION FOR SEQ ID NO: 1:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 2179
41 TYPE: Nucleic acid
42 STRANDEDNESS: Double
43 TOPOLOGY: Linear
44 MOLECULE TYPE: cdna to mRNA
45 ORIGINAL SOURCE:
46 ORGANISM: Homo sapiens
47 TISSUE TYPE: Testis
48 IMMEDIATE SOURCE:
49 LIBRARY: 19t11 cdna library, Clontech #HL1010b
50 CLONE: pFHSR11-11, pFHSR15-6
51 FEATURE:
52 NAME/KEY: protein coding region
53 LOCATION: 75 to 2159
54 US-08-482-855-1

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Query Match 100.0%; Score 18; DB 3; Length 2179;

Best Local Similarity 66.7%; Pred. No. 0.21;  
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0

Qy 1 AUAUUAUGGCCUGCUC 18  
|:|:|:|:|:|:|:|:  
Db 69 ATAATTATGGCCCTGCTC 86

RESULT 4  
US-08-474-986-1  
; Sequence 1, Application US/08474986  
; Patent No. 6372711  
; GENERAL INFORMATION:  
; APPLICANT: Kelton, Christie  
; Schweickhardt, Res  
; Cheng, Shirley Vu  
; Nugent, No. 6372711

;/ TITLE OF INVENTION: Human Follicle Stimulating  
;/ HORMONE RECEPTOR  
;/ NUMBER OF SEQUENCES: 2  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Stephan P. Williams,  
;/ AREA-SERONO, INC.  
;/ STREET: Exchange Place, 37th floor  
;/ CITY: Boston  
;/ STATE: MA  
;/ COUNTRY: USA  
;/ ZIP: 02109  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
;/ COMPUTER: IBM PS/2, model 55 SX  
;/ OPERATING SYSTEM: MS-DOS version 4.0  
;/ SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/474,986  
;/ FILING DATE: 07-Jun-1995  
;/ CLASSIFICATION: <Unknown>  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/670,085  
;/ FILING DATE: <Unknown>  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Williams, Stephan P.  
;/ REGISTRATION NUMBER: 28546  
;/ REFERENCE/DOCKET NUMBER: US/252  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (617) 723-1300  
;/ TELEFAX: (617) 723-8923  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 2179  
;/ TYPE: Nucleic acid  
;/ STRANDEDNESS: Double  
;/ TOPOLOGY: Linear  
;/ MOLECULE TYPE: cDNA to mRNA  
;/ ORIGINAL SOURCE:  
;/ ORGANISM: Homo sapiens  
;/ TISSUE TYPE: Testis  
;/ IMMEDIATE SOURCE:  
;/ LIBRARY: 19t11 cDNA library, Clontech #HL1010b  
;/ CLONE: pFHSR11-11, pFHSR15-6  
;/ FEATURE:  
;/ NAME/KEY: protein coding region  
;/ LOCATION: 75 to 2159  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
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;/ Query Match 100.0%; Score 18; DB 3; Length 2179;  
;/ Best Local Similarity 66.7%; Pred. No. 0.21;  
;/ Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
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;/ Db 69 ATAATTATGGCCTGCTC 86  
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;/ RESULT 5  
;/ US-09-016-434-1209  
;/ Sequence 1209, Application US/09016434  
;/ Patent No. 6500938  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Janice Au-Young  
;/ APPLICANT: Jeffrey J. Seilhamer  
;/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
;/ TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
;/ NUMBER OF SEQUENCES: 1490  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;/ STREET: 3174 PORTER DRIVE  
;/ CITY: PALO ALTO  
;/ STATE: CALIFORNIA

;/ COUNTRY: USA  
;/ ZIP: 94304  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/016,434  
;/ FILING DATE: HERewith  
;/ CLASSIFICATION:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER:  
;/ FILING DATE:  
;/ CLASSIFICATION:  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Zeller, Karen J.  
;/ REGISTRATION NUMBER: 37,071  
;/ REFERENCE/DOCKET NUMBER: PA-0002 US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (650) 855-0555  
;/ TELEFAX: (650) 845-4166  
;/ INFORMATION FOR SEQ ID NO: 1209:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 2393 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ IMMEDIATE SOURCE:  
;/ LIBRARY: GENBANK  
;/ CLONE: g182770  
;/ US-09-016-434-1209  
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;/ Query Match 100.0%; Score 18; DB 3; Length 2393;  
;/ Best Local Similarity 66.7%; Pred. No. 0.21;  
;/ Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
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;/ Db 61 ATAATTATGGCCTGCTC 78  
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;/ RESULT 6  
;/ US-09-270-767-1666  
;/ Sequence 1666, Application US/09270767  
;/ Patent No. 6703491  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Homburger et al.  
;/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
;/ FILE REFERENCE: File Reference: 7326-094  
;/ CURRENT APPLICATION NUMBER: US/09/270,767  
;/ CURRENT FILING DATE: 1999-03-17  
;/ NUMBER OF SEQ ID NOS: 62517  
;/ SOFTWARE: Patentin Ver. 2.0  
;/ SEQ ID NO 1666  
;/ LENGTH: 481  
;/ TYPE: DNA  
;/ ORGANISM: Drosophila melanogaster  
;/ US-09-270-767-1666  
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;/ Query Match 83.3%; Score 15; DB 3; Length 481;  
;/ Best Local Similarity 66.7%; Pred. No. 12;  
;/ Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
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;/ :|||:|||||:  
;/ Db 185 ATTATGGCCTGCTC 199  
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;/ RESULT 7  
;/ US-09-270-767-16948  
;/ Sequence 16948, Application US/09270767  
;/ Patent No. 6703491

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7328-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16948
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16948

Query Match      83.3%; Score 15; DB 3; Length 481;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      4 AUUAUGGCCUGCUC 18
       |:|:|:|:|:|:|:|:|
Db      185 ATTATGGCCCTGCTC 199

RESULT 8
US-09-949-016-16105/c
; Sequence 16105, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16105
; LENGTH: 52992
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16105

Query Match      83.3%; Score 15; DB 3; Length 52992;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAAUUAUGGCCUG 15
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Db      1241 ATAATTATGGCCCTG 1227

RESULT 9
US-09-489-039A-6996
; Sequence 6996, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6996
; LENGTH: 900
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; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6996

Query Match      77.8%; Score 14; DB 3; Length 900;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      4 AUUAUGGCCUGCU 17
       |:|:|:|:|:|:|:|
Db      124 ATTATGGCCCTGCT 137

RESULT 10
US-09-602-787A-379
; Sequence 379, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schöder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
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; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 379
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1126)
; OTHER INFORMATION: RXN00523
US-09-602-787A-379

Query Match 77.8%; Score 14; DB 3; Length 1149;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 5 UUAUGGCCUGCUC 18
:|||||:
Db 229 TTATGGCCCTGCTC 242

RESULT 11
US-09-620-312D-42/c
; Sequence 42, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radjic T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt\_fl\_genes Version 1.0
; SEQ ID NO 42
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1563)
US-09-620-312D-42

Query Match 77.8%; Score 14; DB 3; Length 1887;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 AUUAUGGCCUGCU 17
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Db 896 ATTATGGCCCTGCT 883

RESULT 12
US-09-112-580-13
; Sequence 13, Application US/09112580
; Patent No. 6610539
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF
; TITLE OF INVENTION: MICROORGANISMS
; FILE REFERENCE: 032396-016
; CURRENT APPLICATION NUMBER: US/09/112,580
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: US 60/052,160
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 265
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Equine herpesvirus 4
US-09-112-580-13

Query Match 77.8%; Score 14; DB 3; Length 3678;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUUGGCCCU 14
|:|||||:
Db 2479 ATAAATTATGGCCCT 2492

RESULT 13
US-09-489-039A-4926/c
; Sequence 4926, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLBBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4926
; LENGTH: 3762
; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1044),(1659)  
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.  
US-09-489-039A-4926

Query Match 77.8%; Score 14; DB 3; Length 3762;  
Best Local Similarity 64.3%; Pred. No. 45;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UUAUGGCCCGCUC 18  
Db 3722 TTATGGCCCTGCTC 3709  
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RESULT 14  
US-09-949-016-15014  
; Sequence 15014, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15014  
; LENGTH: 55264  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15014

Query Match 77.8%; Score 14; DB 3; Length 55264;  
Best Local Similarity 64.3%; Pred. No. 45;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 2 UAAUUAUGGCCUG 15  
Db 41065 TAATTATGGCCCTG 41078  
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RESULT 15  
US-09-949-016-12122/c  
; Sequence 12122, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12122  
; LENGTH: 70828  
; TYPE: DNA  
; ORGANISM: Human

; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(70828)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12122  
Query Match 77.8%; Score 14; DB 3; Length 70828;  
Best Local Similarity 64.3%; Pred. No. 45;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 2 UAAUUAUGGCCUG 15  
Db 35413 TAATTATGGCCCTG 35400  
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Search completed: November 29, 2005, 18:25:00  
Job time : 73 secs



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	18	100.0	441	4	US-09-925-065A-192589	Sequence 192589, App
2	18	100.0	441	4	US-09-925-065A-192590	Sequence 192590, App
3	18	100.0	1922	8	US-10-349-528-4	Sequence 4, Appli
4	18	100.0	2019	7	US-10-382-248-9	Sequence 9, Appli
5	18	100.0	2393	5	US-10-225-567A-121	Sequence 121, Appl
6	18	100.0	2393	5	US-10-207-655-64	Sequence 64, Appl
7	18	100.0	2393	6	US-10-305-920-1209	Sequence 1209, Appl
8	16	88.9	201	8	US-10-719-993-38475	Sequence 38475, A
9	16	88.9	612	4	US-09-925-065A-391076	Sequence 391076, A
10	16	88.9	261638	8	US-10-719-993-6882	Sequence 6882, App
11	15	83.3	461	4	US-09-925-065A-328046	Sequence 328046, App
12	15	83.3	507	6	US-10-172-118-2085	Sequence 2085, App
13	15	83.3	507	7	US-10-342-887-2095	Sequence 2095, App
14	15	83.3	533	4	US-09-925-065A-520324	Sequence 520324, A
15	15	83.3	544	4	US-09-925-065A-539398	Sequence 539398, A
16	15	83.3	612	5	US-10-007-280A-106	Sequence 106, Appl
17	15	83.3	628	5	US-10-007-280A-107	Sequence 107, Appl
18	15	83.3	842	5	US-10-027-632-160723	Sequence 160723, A
19	15	83.3	842	5	US-10-027-632-160724	Sequence 160724, A
20	15	83.3	842	6	US-10-027-632-160723	Sequence 160723, A
21	15	83.3	842	6	US-10-027-632-160724	Sequence 160724, A
22	15	83.3	1634	7	US-10-424-599-84619	Sequence 84619, A
23	15	83.3	2021	8	US-10-739-930-4619	Sequence 4619, App

## ALIGNMENTS

FILE REFERENCE: 108627.133  
CURRENT APPLICATION NUMBER: IIS/09/925.065A

; CURRENT FILING DATE: 2001-08-08  
 ; REGISTRATION NUMBER: US 60/242 086

; PRIOR FILING DATE: 2000-10-24

;  
; PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

;; PRIOR APPLICATION NUMBER: US 60/289,940  
PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SEQ ID NO 192589

TYPE: DNA

US-09-925-065A-192589

Query Match 100.0% Score 18:

BEST LOCAL SIMILARITY 66.7%; FREQ. NO.  
VARIABLE 12. Concentration 6. Migration

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[illegible]

## RESULT 2

03-03-923-003A-122330 : Sequence 192590 Application IIS/09925065A

Publication No. US20050228172A9

APPLICANT: Wang, David G.

; TITLE OF INVENTION: Nucleotide Polymorph



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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-64

Query Match      100.0%; Score 18; DB 5; Length 2393;
Best Local Similarity 66.7%; Pred. No. 0.48;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUAGGCCCGCUC 18
Db 61 ATAATTATGGCCCTGCTC 78

RESULT 7
US-10-305-720-1209
; Sequence 1209, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1209
; LENGTH: 2393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g182770
US-10-305-720-1209

Query Match      100.0%; Score 18; DB 6; Length 2393;
Best Local Similarity 66.7%; Pred. No. 0.48;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUAGGCCCGCUC 18
Db 61 ATAATTATGGCCCTGCTC 78

RESULT 8
US-10-719-993-38475
; Sequence 38475, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38475
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-38475

Query Match      88.9%; Score 16; DB 8; Length 201;
Best Local Similarity 68.8%; Pred. No. 7.7;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUAGGCCCGCUC 16
Db 113 ATAATTATGGCCCTGCTC 128
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RESULT 9
US-09-925-065A-391076
; Sequence 391076, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391076
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-391076

Query Match      88.9%; Score 16; DB 4; Length 612;
Best Local Similarity 62.5%; Pred. No. 7.8;
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAAUAUAGGCCCGCUC 17
Db 565 TAATTATGGCCCTGCT 580

RESULT 10
US-10-719-993-6882
; Sequence 6882, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6882
; LENGTH: 261638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6882

Query Match      88.9%; Score 16; DB 8; Length 261638;
Best Local Similarity 68.8%; Pred. No. 8.4;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUAGGCCCGCUC 16
Db 29139 ATAATTATGGCCCTGCTC 29154

RESULT 11
US-09-925-065A-328046
; Sequence 328046, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

```
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328046
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-328046
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```
Query Match      83.3%; Score 15; DB 4; Length 461;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 AAUUAUGGCCCGCU 17
        ||:::||::||::||:
Db      11 AATTATGGCCCTGCT 25
```

```
RESULT 12
US-10-172-118-2085/c
; Sequence 2085, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Contig23454
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2085
```

```
Query Match      83.3%; Score 15; DB 6; Length 507;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 AAUUAUGGCCCGCU 17
        ||:::||::||::||:
Db      177 AATTATGGCCCTGCT 163
```

```
RESULT 13
US-10-342-887-2085/c
; Sequence 2085, Application US/10342887
; Publication No. US20040058340A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-2085
```

```
Query Match      83.3%; Score 15; DB 7; Length 507;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 AAUUAUGGCCCGCU 17
        ||:::||::||::||:
Db      177 AATTATGGCCCTGCT 163
```

```
RESULT 14
US-09-925-065A-520324/c
; Sequence 520324, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 520324
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-520324
```

```
Query Match      83.3%; Score 15; DB 4; Length 533;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 AAUUAUGGCCCGCU 17
        ||:::||::||::||:
Db      368 AATTATGGCCCTGCT 354
```

```

RESULT 15
US-09-925-065A-539398/c
; Sequence 539398, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 539398
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539398

```

```

Query Match      83.3%; Score 15; DB 4; Length 544;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 AAUUAUGGCCUCCU 17
Db      368 AATTATGGCCCTGCT 354

```

```

Search completed: November 29, 2005, 20:39:07
Job time : 404.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:25:08 ; Search time 894.5 Seconds  
(without alignments)  
1143.859 Million cell updates/sec

Title: US-10-018-716B-2

Perfect score: 18  
Sequence: 1 auaauauggcccguc 18

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sta.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	856	8 HSFSTHR	X68044 H.sapiens m
2	18	100.0	1724	8 S73199	S73199 follicle-st
3	18	100.0	1734	8 HSFSTHR	234260 H.sapiens D
4	18	100.0	2179	6 AR003719	AR003719 Sequence
5	18	100.0	2179	6 AR067576	AR067576 Sequence
6	18	100.0	2179	6 AR207283	AR207283 Sequence
7	18	100.0	2179	8 S59900	S59900 follicle st
8	18	100.0	2186	8 HUMFSHRE	M95489 H.sapiens f
9	18	100.0	2222	6 A76125	A76125 Sequence 1
10	18	100.0	2374	6 CQ715054	CQ715054 Sequence
11	18	100.0	2393	6 AR270646	AR270646 Sequence
12	18	100.0	2393	6 AX548836	AX548836 Sequence
13	18	100.0	2393	8 HUMFSHRE	M65085 Human folli
14	18	100.0	121688	8 AC092533	AC092533 Homo sapi
15	18	100.0	158709	14 AC083827	AC083827 Homo sapi
16	17	94.4	162	8 HSFSTHR	X91738 H.sapiens g
17	16	88.9	1041	5 AY625217	AY625217 Priotelus
18	16	88.9	95681	8 AL157890	AL157890 Human DNA

19	16	88.9	113657	14	AC166226	AC166226 Sorex ara
20	16	88.9	121589	14	AC137655	AC137655 Bos tauru
21	16	88.9	125311	8	AC068758	AC068758 Homo sapi
22	16	88.9	127015	14	AC151504	AC151504 Dasytus n
23	16	88.9	160179	14	AC092930	AC092930 Homo sapi
24	16	88.9	168380	8	AC063933	AC063933 Homo sapi
25	16	88.9	169314	14	AC148413	AC148413 Callithri
26	16	88.9	169996	14	AC053521	AC053521 Homo sapi
27	16	88.9	171267	14	AC154087	AC154087 Alligator
28	16	88.9	171990	14	AC153783	AC153783 Rhinolph
29	16	88.9	185798	14	AC158248	AC158248 Callithri
30	16	88.9	187465	9	AC132305	AC132305 Mus muscu
31	16	88.9	191709	9	AC115890	AC115890 Mus muscu
32	16	88.9	197909	9	AC158658	AC158658 Mus muscu
33	16	88.9	198551	9	AC068605	AC068605 Mus muscu
34	16	88.9	210236	14	AC150699	AC150699 Bos tauru
35	16	88.9	236157	14	AC111356	AC111356 Rattus no
36	16	88.9	256499	14	AC130987	AC130987 Rattus no
37	16	88.9	283919	14	AC095169	AC095169 Rattus no
38	15	83.3	481	6	AR496706	AR496706 Sequence
39	15	83.3	481	6	AR511988	AR511988 Sequence
40	15	83.3	612	6	AX554759	AX554759 Sequence
41	15	83.3	628	6	AX554760	AX554760 Sequence
42	15	83.3	1303	5	CR760514	CR760514 Xenopus t
43	15	83.3	1437	5	BC061373	BC061373 Xenopus t
44	15	83.3	1727	15	AB023467	AB023467 Mettechni
45	15	83.3	2652	8	BC034230	BC034230 Homo sapi

ALIGNMENTS

RESULT 1	HSFSTHR	H.sapiens mRNA for follicle-stimulating hormone receptor.	856 bp	mRNA	linear	PRI 07-FEB-1993
LOCUS	X68044					
DEFINITION	X68044.1	GI:31473				
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
CDS						





JOURNAL	Mol. Cell. Endocrinol.	89 (1-2), 141-151 (1992)
PUBMED	1301382	
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbon 130880] from the original journal article.	
FEATURES	Location/Qualifiers	
source	1..2179	/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="taxon:9606"
gene	1..2179	/gene="follicle stimulating hormone receptor, FSH receptor"
CDS	75..2162	/gene="follicle stimulating hormone receptor, FSH receptor"
		/codon_start=1
		/product="follicle stimulating hormone receptor"
		/protein_id="AAB26480.1"
		/db_xref="GI:300073"
		/translation="MALLLVSLAPLSLGSCHHRICHCSNRVFLCQESKVTETSPDIPRNLAEFLVTKLRVIQKGFSGFDELEKIEISQNDVLEVIEDVFNPLKLEIRIENANLLYNPEAFONLNQVLIHSNKHLPDVHKHSLOKLVDIQDNINIHGISENSFVLSESVILMNKGIOETHNCAFNQTDLDELNNNLBELPNDVPFHGASGPVIDISRTRHSLPSYGLNKLRARSTYNLKUPTLEKLVAMEASTLYFSHCCEAFANRRROISELHPICNKSIQRVEDVNTQTRGRSSLAEDNESSYRGPDMTYTEFYDLCNEVDVTCSPKPDAFPNCEDIINGYNILRVLFITSLAITGNIVLVLTTSQKUTVRFLMCNLAFADLCIGYLLLIASVDITHKSQHNYAIDWQTGCAGCGAFTVFASLSVTLTAITLERWHITTAMQLDCVKQLRAASVMVGWIFAPAALPIFGSSYMKVSYICLPMDDISPLSQYMSLVLNVLAFLVLCGCVIHLVLTVRNPNIYSSSSDTRIARKMALIFTDFLCWAFISFAISASKVLITVSKAKILLVLFHPINSANCSPFYAIPTKNFRDRDFILLSKGCGYEMQAQIYRTTSTVHNTHPRNGHCSAPPRTVNGSGSTYLVLPSHLAQN"
ORIGIN		
Query Match	100.0%;	Score 18; DB 8; Length 2179;
Best Local Similarity	66.7%;	Pred. No. 5.6;
Matches	12; Conservative	6; Mismatches 0; Indels 0; Gaps 0;
Qy	1 AUAUUUUGGCCCGUCUC 18	
	: ::   ::   :	
Db	69 ATAATTATGGCCCTGCTC 86	
	: ::   ::   :	
RESULT 8		
HUMFSHREC		
LOCUS	2186 bp mRNA linear PRI 08-NOV-1999	
DEFINITION	H.sapiens follicle stimulating hormone receptor mRNA, complete cds	
ACCESSION	M95489	
VERSION	M95489.1 GI:182772	
KEYWORDS	G-protein coupled receptor; follicle stimulating hormone (FSH) receptor.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 2186)	
AUTHORS	Tilly,L.T., Ahara,T., Nishimori,K., Jai,X., Billig,H., Kowalski,K.I., Perlas,E.A. and Heueh,A.J.W.	
TITLE	Expression of recombinant human follicle-stimulating hormone receptor: Species-specific ligand binding, signal transduction, and identification of multiple ovarian messenger ribonucleic acid transcripts	
JOURNAL	Endocrinology (1992) In press	
COMMENT	Original source text: Homo sapiens male adult testis cDNA to mRNA.	
FEATURES	Location/Qualifiers	
source	1..2186	/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/map="Unassigned"
		/sex="male"





Center project name: H\_NH0057110  
Drafting Center: WIBR

NOTICE:

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >= 30);  
an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,  
Department of Genetics, Washington University, St. Louis MO. For  
additional information about the map position of this sequence, see  
http://genome.wustl.edu

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male  
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,  
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved  
approach for construction of bacterial artificial chromosome  
libraries. Genomics 51:1-8. The clone may be obtained either from  
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong  
and coworkers at http://www.chori.org  
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-125F24, 2000 bp overlap.  
Actual start of this clone is at base position 9748 of RP11-125F24;  
actual end is at base position 121688 of RP11-57110.

The sequence of AC027148 has been incorporated into AC092533.

FEATURES  
Source

1..121688  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/clone="RP11-57110"  
/clone\_lib="RPCI-11"  
complement(82833..83058)  
/gene="FSHR"  
complement(82833..83058)  
/gene="FSHR"  
complement(<82833..82984)  
/gene="FSHR"  
/note="Homo sapiens follicle stimulating hormone receptor  
(FSHR), transcript variant 1, mRNA.; H\_NH0057110.1  
This gene was based on GI(31657137)  
Continues as H\_NH0125F24.1"  
/codon\_start=1  
/product="unknown"  
/protein\_id="AA88895.1"  
/db\_xref="GI:62630150"  
/translation="MALLLVSLAFLSLGSGCHRHICHSNRVFLCQESKVTIIPSDL  
PRNAIEL"

gene

mRNA

CDS

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 121688;  
Best Local Similarity 66.7%; Pred. No. 5.6;  
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUUUAGGCCUGUC 18

|:|:|:|:|:|:|:|:|

Db 82990 ATAATTATGGCCCTGTC 82973

RESULT 15  
AC083827/c

LOCUS AC083827 158709 bp DNA linear HTG 24-JAN-2002  
DEFINITION Homo sapiens chromosome 2 clone RP11-345C21, WORKING DRAFT  
SEQUENCE, 23 unordered pieces.  
ACCESSION AC083827  
VERSION AC083827.2 GI:15375221  
KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 158709)  
AUTHORS Waterston, R.H.  
TITLE The sequence of Homo sapiens clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 158709)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (02-OCT-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
COMMENT On Aug 30, 2001 this sequence version replaced gi:10445290.  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
Contact: submissions@wustl.edu  
----- Project Information -----  
Center project name: H\_NH0345C21  
----- Summary Statistics -----  
Sequencing vector: M13, 100%  
Sequencing vector: plasmid, 0%  
Chemistry: Dye-Primer ET; 8% of reads  
Chemistry: Dye-Terminator Big Dye; 92% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 142571 bases at least Q40  
Consensus quality: 147681 bases at least Q30  
Consensus quality: 150874 bases at least Q20  
Insert size: 167000; agarose-fp  
Insert size: 156781; sum-of-contigs  
Quality coverage: 3.10 in Q20 bases; agarose-fp  
Quality coverage: 3.36 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 23 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 1192: contig of 1192 bp in length  
\* 1193 1292: gap of unknown length  
\* 1293 2772: contig of 1480 bp in length  
\* 2773 2873: gap of unknown length  
\* 2873 4402: contig of 1529 bp in length  
\* 4402 4503: gap of unknown length  
\* 4503 4502: contig of 2252 bp in length  
\* 4502 6753: gap of unknown length  
\* 6753 6854: contig of 1910 bp in length  
\* 6854 8763: gap of unknown length  
\* 8763 8864: contig of 2200 bp in length  
\* 8864 11063: gap of unknown length  
\* 11063 11164: contig of 2989 bp in length  
\* 11164 14152: gap of unknown length  
\* 14152 14252: gap of unknown length  
\* 14252 17321: contig of 3069 bp in length  
\* 17321 17421: gap of unknown length  
\* 17421 19872: contig of 2451 bp in length  
\* 19872 19973: gap of unknown length  
\* 19973 22887: contig of 2914 bp in length  
\* 22887 22986: gap of unknown length



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Result No.	Score	Query			DB	ID	Description
		Match	Length	Length			
C	1	18	100.0	18	4	AAC90409	Aac90409 Human FSH
	2	18	100.0	18	4	AAC90408	Aac90408 Human FSH
	3	18	100.0	1922	11	ADP03559	Adp03559 Human GPC
	4	18	100.0	2019	10	ADC24202	Adc24202 Human NOV
5	18	100.0	2179	2	AAT63181	Aat63181 FSH recep	
6	18	100.0	2180	2	AAQ29377	Aaq29377 FSH recep	
7	18	100.0	2222	2	AAQ50013	Aaq50013 FSH recep	
8	18	100.0	2393	8	ABZ42665	Abz42665 Human fol	
9	18	100.0	2393	10	ADD25503	Add25503 Binding d	
10	18	100.0	2393	10	ACA56611	Aca56611 Human sig	
11	18	100.0	2393	12	AD156407	Ad156407 Human pol	
12	18	100.0	2393	12	ADO29879	Ado29879 Human GPC	
C	13	15	83.3	507	13	ADR26224	Adr26224 Breast ca
	14	15	83.3	612	6	ABT03390	Abt03390 Ovary cel
	15	15	83.3	628	6	ABT03391	Abt03391 Ovary cel
16	15	83.3	2021	13	ADT13293	Adt13293 Plant cDN	
17	15	83.3	3659	4	ABL12007	Ab112007 Drosophi	
C	18	15	83.3	8253	13	ADR84405	Adr84405 Apterogill
	19	15	83.3	9140	4	ABL12006	Ab112006 Drosophi
	20	15	83.3	9140	4	ABL12006	Ab112006 Drosophi

AA The present invention relates to a composition, which comprises at least  
CC one antisense oligonucleotide that is complementary to follicle-  
CC stimulating hormone receptor (FSHR) coding sequence. The present sequence  
CC is one such oligonucleotide used in the composition. The composition of  
CC the present invention can be used for regulating hormones of a host. The





CC which was isolated by the method of the invention.

XX Sequence 1922 BP; 499 A; 504 C; 387 G; 532 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 18; DB 11; Length 1922;  
Best Local Similarity 66.7%; Pred. No. 1.3;  
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUUUAGGCCUGCUC 18

Db 11 ATAATTATGGCCCTGCTC 28

RESULT 4

ADC24202

ID ADC24202 standard; cDNA; 2019 BP.

XX ADC24202;

AC ADC24202;

DT 18-DEC-2003 (first entry)

XX Human NOV3a encoding cDNA SEQ ID NO:9.

XX human; NOVX; cardiac; antiarteriosclerotic; hypotensive; vasotropic;  
KW dermatological; anorectic; immunosuppressive; cytostatic;  
KW antiinfertility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory;  
KW neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy;  
KW cardiomyopathy; atherosclerosis; hypertension; congenital heart defect;  
KW pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity;  
KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;  
KW prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma;  
KW fertility; haemophilia; graft versus host disease; AIDS;  
KW bronchial asthma; Crohn's disease; multiple sclerosis;  
KW infectious disease; anorexia; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 61..1962

FT /\*tag= a

FT /product= "NOV3a"

XX WO2003076584-A2.

XX 18-SEP-2003.

XX 06-MAR-2003; 2003WO-US006951.

XX 06-MAR-2002; 2002US-0361974P.

XX 19-MAR-2002; 2002US-0365477P.

XX 22-MAR-2002; 2002US-0366928P.

XX 06-AUG-2002; 2002US-0401661P.

XX 05-MAR-2003; 2003US-00401661.

XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Burgess CE, Edinger SR, Gerlach VL, Ji W, Kekuda R;

XX Li L, Macdougall JR, Miller CE, Millet I, Patturajan M, Pena CE;

XX Rieger DK, Sciore P, Shenoy SG, Smithson G, Spytek KA, Stone DJ;

XX Voss EZ, Zhong M;

XX WPI; 2003-722330/68.

XX P-PSDB; ADC24203.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing or  
PT treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,  
PT obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or  
PT multiple sclerosis.

PS Claim 20; SEQ ID NO 9; 229pp; English.

XX

CC The present invention describes novel human proteins, designated NOVX  
CC proteins. The NOVX sequences have cardiac, antiarteriosclerotic,  
CC hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,  
CC cytostatic, antiinfertility, haemostatic, anti-HIV, antiasthmatic,  
CC antiinflammatory, neuroprotective, anabolic, nootropic and  
CC antiparkinsonian activities, and can be used in gene therapy. The NOVX  
CC sequences can be used as a therapeutic in the manufacture of a medicament  
CC for treating a syndrome associated with a human disease, such as a  
CC pathology associated with NOVX. The NOVX proteins and nucleic acids  
CC encoding them are useful for diagnosing or treating pathologies, diseases  
CC or conditions associated with NOVX sequences, including cardiomyopathy,  
CC atherosclerosis, hypertension, congenital heart defects, pulmonary  
CC stenosis, scleroderma, obesity, metabolic disturbances associated with  
CC obesity, transplantation, adrenoleukodystrophy, congenital adrenal  
CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,  
CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,  
CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious  
CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,  
CC or Parkinson's disease), immune disorders, haematopoietic disorders,  
CC dyslipidaemias, and wasting disorders associated with chronic diseases.  
CC The proteins can also be used as immunogens to produce antibodies and as  
CC vaccines. The sequences may further be used in chromosome mapping,  
CC identifying individual from minute biological samples (tissue typing),  
CC and in forensic identification of a biological sample. The present  
CC sequence encodes human NOV3a from the present invention.

XX Sequence 2019 BP; 527 A; 514 C; 411 G; 567 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 18; DB 10; Length 2019;

Db Best Local Similarity 66.7%; Pred. No. 1.3;

Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUUUAGGCCUGCUC 18

Db 55 ATAATTATGGCCCTGCTC 72

RESULT 5

AAT63181

ID AAT63181 standard; DNA; 2179 BP.

XX AAT63181;

XX 20-JUN-1997 (first entry)

XX FSH receptor gene wild-type allele.

XX Follicle stimulating hormone receptor; FSH receptor; ovarian dysgenesis;

XX hypergonadotropic hypogonadism; diagnosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT exon 70..227

FT /\*tag= c

FT /note= "nucleotides 70-227 correspond to nucleotides 1-

FT 158 of fshr exon 1"

FT CDS 75..2159

FT /\*tag= a

FT exon 228..298

FT /\*tag= c

FT /note= "nucleotides 228-298 correspond to nucleotides 7-

FT 77 of fshr exon 2"

FT exon 299..373

FT /\*tag= c

FT /note= "nucleotides 299-373 correspond to nucleotides 6-

FT 80 of fshr exon 3"

FT exon 374..450

FT /\*tag= c

FT /note= "nucleotides 374-450 correspond to nucleotides 6-

FT 82 of fshr exon 4"

FT exon 451..520

FT /\*tag= c

FT

```

FT /note= "nucleotides 451-520 correspond to nucleotides 8-
FT 77 of fshr exon 5"
FT 521..598
FT /*tag= c
FT /note= "nucleotides 521..598 correspond to nucleotides 6-
FT 83 of fshr exon 6"
FT 599..668
FT /*tag= c
FT /note= "nucleotides 599-668 correspond to nucleotides 6-
FT 75 of fshr exon 7"
FT 640
FT /*tag= b
FT /note= "a C to T mutation in codon 189 correlates with
FT ovarian dysgenesis"
FT 669..742
FT /*tag= c
FT /note= "nucleotides 669-742 correspond to nucleotides 7-
FT 80 of fshr exon 8"
FT 743..928
FT /*tag= c
FT /note= "nucleotides 743-928 correspond to nucleotides 6-
FT 191 of fshr exon 9"
FT 929..2179
FT /*tag= c
FT /note= "nucleotides 929-2179 correspond to nucleotides
FT 102-1352 of fshr exon 10"
FT
FT
XX WO9711194-A1.
PN
XX
XX
XX 27-MAR-1997.
PD
XX
XX 20-SEP-1996; 96WO-FI000501.
PF
XX
XX 20-SEP-1995; 95US-00531070.
PR
XX
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PA
XX
XX De La Chapelle A, Aittomaeki K, Huhtaniemi I;
XX
XX WPI; 1997-202900/18.
DR
XX P-PSDB; AAW14782.
XX
XX Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities - by
XX amplifying DNA including follicle stimulating hormone receptor allele(s),
XX i.e. codon 189, cleaving fragments, and examination.
XX
XX Claim 17; Page 18-21; 43pp; English.
XX
XX A DNA sequence (AAT63181) comprises the coding region from exons 1-10 of
XX the wild-type fshr gene that codes for human follicle stimulating hormone
XX (FSH) receptor (AAW14782). A C to T mutation in exon 7 (codon 189) is
XX associated with ovarian dysgenesis. In a method for determining a FSH
XX receptor genotype in a human patient, fshr exon 7, or a portion of it, is
XX isolated by PCR amplification (see also AAT63195-96) and exposed to BsmI.
XX Exon 7 contains a unique BsmI site which, if mutated, will produce no
XX BsmI digestion products, thereby enabling diagnosis of ovarian dysgenesis
XX
XX Sequence 2179 BP; 575 A; 561 C; 444 G; 599 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 2; Length 2179;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUUUAUGGCCUGCUC 18
Db |||:|||||:|
69 ATAATTATGGCCCTGCTC 86

RESULT 6
AAQ29377
ID AAQ29377 standard; DNA; 2180 BP.
XX
XX
XX AAQ29377;
AC

```

```

XX 25-MAR-2003 (revised)
DT 04-MAR-1993 (first entry)
XX
XX FSHR DNA.
DE
XX Human; follicle stimulating hormone receptor; maturation;
XX spermatogenesis; birth control; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 75..2159
XX /*tag= a
XX sig_peptide 75..126
XX /*tag= b
XX mat_peptide 127..2159
XX /*tag= c
XX
XX WO9216620-A1.
XX
XX 01-OCT-1992.
PD
XX
XX 02-JAN-1992; 92WO-US000122.
PF
XX
XX 15-MAR-1991; 91US-00670085.
PR
XX
XX (ISTF ) ARS APPL RES SYST HOLDING NV.
XX
XX Kelton CA, Cheng SVY, Nugent NP, Schweickhardt RL;
XX
XX WPI; 1992-349206/42.
DR
XX P-PSDB; AAR29377.
XX
XX Pure human FSH receptor, fragments and mutants - for preventing follicle
XX growth, maturation and spermatogenesis, also for use of appropriate cell
XX lines for bio-assays of FSH.
XX
XX Claim 7; Page 25; 48pp; English.
XX
XX The DNA sequence encoding human follicle stimulating hormone receptor
XX (FSHR) was obtd. by screening a lambda gtl1 cDNA library constructed from
XX RNA extracted from human testis and amplified, with a rat FSHR cDNA clone
XX as a probe. Positive colonies were used for a secondary screen which
XX isolated five putative human FSHR clones. None of the clones contained
XX the complete hFSHR coding region but could be overlapped using GCG to
XX give the complete sequence. hFSHR binds to FSH to reduce endogenous FSH
XX bioactivity, in females to prevent follicle growth and maturation and in
XX CC males to prevent spermatogenesis, i.e. as a birth control agent. (Updated
XX on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 2180 BP; 577 A; 560 C; 444 G; 599 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 2; Length 2180;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUUUAUGGCCUGCUC 18
Db |||:|||||:|
70 ATAATTATGGCCCTGCTC 87

RESULT 7
AAQ50013
ID AAQ50013 standard; cDNA to mRNA; 2222 BP.
XX
XX
XX AAQ50013;
XX
XX 25-MAR-2003 (revised)
DT 05-MAY-1994 (first entry)
XX
XX FSH receptor.
DE
XX

```





OS Homo sapiens.  
 XX US2004010136-A1.  
 PN  
 XX  
 XX  
 PD 15-JAN-2004.  
 XX  
 XX  
 PF 26-NOV-2002; 2002US-00305720.  
 XX  
 XX 30-JAN-1998; 98US-00016434.  
 PR  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX  
 XX Au-Young J, Seilhamer JG;  
 PI  
 XX WPI; 2004-090520/09.  
 DR  
 XX  
 XX  
 XX New composition comprising polynucleotide probes, useful as array  
 PT elements in a microarray for monitoring the expression of target  
 PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
 PT fragments.  
 XX  
 XX Claim 6; SEQ ID NO 1209; 73pp; English.  
 PS  
 XX  
 XX The invention relates to a composition of polynucleotide probes  
 CC comprising first polynucleotide probes comprising at least a portion of a  
 CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
 CC comprising at least a portion of a gene encoding a transducing  
 CC polypeptide and third polynucleotide probes comprising at least a portion  
 CC of a gene encoding an effector-like polypeptide. The probes of the  
 CC composition are useful as array elements in a microarray for monitoring  
 CC the expression of target polynucleotides. The microarray is useful in the  
 CC diagnosis and treatment of cancer, an immunopathology or a  
 CC neuropathology. It can also be used for drug discovery and development.  
 CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.  
 CC Microarrays can also be used for monitoring the progression of diseases  
 CC that may be associated with the altered expression of signalling pathway  
 CC polypeptides. The composition can also be used to purify a subpopulation  
 CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
 CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of  
 CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
 CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
 CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
 CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
 CC human polynucleotide probe of the invention. Note: The sequence data for  
 CC this patent did not form part of the printed specification but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 XX Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 18; DB 12; Length 2393;  
 Best Local Similarity 66.7%; Pred.No. 1.3;  
 Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AUAUUAUAGGCCGUCUC 18  
 Db :|||:|||||:  
 61 ATAATTATGCGCTGCTC 78  
 RESULT 12  
 ADO29879  
 ID ADO29879 standard; cDNA; 2393 BP.  
 XX  
 AC ADO29879;  
 XX  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX Human GPCR FSHR polynucleotide, SEQ ID NO:981.  
 DE  
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;

KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianic;  
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW viricide; hepatotropic; antibacterial; antianemic; antiseborrheic;  
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KW gene; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2004040000-A2.  
 PN  
 XX 13-MAY-2004.  
 PD  
 XX 09-SEP-2003; 2003WO-US028226.  
 XX  
 PF 09-SEP-2002; 2002US-0409303P.  
 XX  
 PR 09-APR-2003; 2003US-0461329P.  
 XX  
 XX (PRIM-) PRIMAL INC.  
 PA  
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
 XX  
 XX WPI; 2004-390329/36.  
 DR  
 DR F-PSDB; ADO29321.  
 XX  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX  
 PS Claim 151; SEQ ID NO 981; 542pp; English.  
 XX  
 XX The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridise to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 CC nucleic acid of the invention. Note: The full sequence data for this  
 CC patent did not form part of the printed specification; those sequences  
 CC not shown were obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 12; Length 2393;

```
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUAGGCCUGUC 18
Db 61 AATATTATGCGCCCTGCTC 78

RESULT 13
ADR26224/c
ID ADR26224 standard; DNA; 507 BP.
XX
AC ADR26224;
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #2085.
XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
DR WPI; 2004-593473/57.
XX
PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
PS Disclosure; SEQ ID NO 2085; 226pp; English.
XX
CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
SQ Sequence 507 BP; 151 A; 103 C; 90 G; 163 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 13; Length 507;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUAUAGGCCUGUCU 17
Db 177 AATTATGCGCCCTGCT 163

RESULT 14
ABT03390
ID ABT03390 standard; DNA; 612 BP.
XX
AC ABT03390;
XX
DT 28-NOV-2002 (first entry)
XX

Query Match 83.3%; Score 15; DB 13; Length 507;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUAUAGGCCUGUCU 17
Db 177 AATTATGCGCCCTGCT 163

RESULT 15
ABT03391
ID ABT03391 standard; DNA; 628 BP.
XX
AC ABT03391;
XX
DT 28-NOV-2002 (first entry)
XX
DE Ovary cell-specific DNA sequence 107.
XX
KW Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200238606-A2.
XX
PD 16-MAY-2002.
XX
PF 07-NOV-2001; 2001WO-US046459.
XX
PR 08-NOV-2000; 2000US-0246640P.
XX

DE Ovary cell-specific DNA sequence 106.
XX
KW Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200238606-A2.
XX
PD 16-MAY-2002.
XX
PF 07-NOV-2001; 2001WO-US046459.
XX
PR 08-NOV-2000; 2000US-0246640P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Recipon H, Salceda S, Liu C;
XX
DR WPI; 2002-519297/55.
XX
PT Polypeptide and polynucleotides present in normal and neoplastic ovary
PT cells, useful for identifying, monitoring, staging, diagnosing,
PT preventing and treating ovarian cancer, and non-cancerous disease states
PT in the ovary.
XX
PS Claim 1; Page 192; 247pp; English.
XX
CC The invention comprises amino acid and DNA sequences which are present in
CC normal and neoplastic ovary cells. The DNA and protein sequences of the
CC invention are useful for determining the presence of an ovary specific
CC nucleic acid or an ovary specific protein in a sample. The DNA and
CC protein sequences of the invention are useful for diagnosing and
CC monitoring the presence and metastasis of ovarian cancer and breast
CC cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell
CC specific DNA sequences of the invention
XX
SQ Sequence 612 BP; 202 A; 112 C; 108 G; 190 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 612;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUAUAGGCCUGUCU 17
Db 289 AATTATGCGCCCTGCT 303

RESULT 15
ABT03391
ID ABT03391 standard; DNA; 628 BP.
XX
AC ABT03391;
XX
DT 28-NOV-2002 (first entry)
XX
DE Ovary cell-specific DNA sequence 107.
XX
KW Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200238606-A2.
XX
PD 16-MAY-2002.
XX
PF 07-NOV-2001; 2001WO-US046459.
XX
PR 08-NOV-2000; 2000US-0246640P.
XX
```

PA (DIAD-) DIADEXUS INC.  
XX  
PI Sun Y, Recipon H, Salceda S, Liu C;  
XX  
DR WPI; 2002-519297/55.  
XX  
PT Polypeptide and polynucleotides present in normal and neoplastic ovary  
PT cells, useful for identifying, monitoring, staging, diagnosing,  
PT preventing and treating ovarian cancer, and non-cancerous disease states  
PT in the ovary.  
XX  
PS Claim 1; Page 192-193; 247pp; English.  
XX  
CC The invention comprises amino acid and DNA sequences which are present in  
CC normal and neoplastic ovary cells. The DNA and protein sequences of the  
CC invention are useful for determining the presence of an ovary specific  
CC nucleic acid or an ovary specific protein in a sample. The DNA and  
CC protein sequences of the invention are useful for diagnosing and  
CC monitoring the presence and metastasis of ovarian cancer and breast  
CC cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell  
CC specific DNA sequences of the invention  
XX  
SQ Sequence 628 BP; 202 A; 115 C; 102 G; 209 T; 0 U; 0 Other;  
  
Query Match 83.3%; Score 15; DB 6; Length 628;  
Best Local Similarity 66.7%; Pred. No. 64;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 AATUUGGCCUCCU 17  
||:::||::||:  
Db 305 AATTATGGCCCTGCT 319

Search completed: November 29, 2005, 23:12:28  
Job time : 223.5 secs

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# OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:29:48 ; Search time 1867.5 Seconds  
(without alignments)  
450.960 Million cell updates/sec

Title: US-10-018-716B-1

Perfect score: 18

Sequence: 1 gacgagggccataattat 18

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

## Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	94.4	794	1	AJ641058
2	16	88.9	312	2	BE153987
3	16	88.9	340	3	BI432519
4	16	88.9	439	8	T14826
5	16	88.9	500	3	BP191026
6	16	88.9	652	2	BG600462
7	16	88.9	740	8	CX409188
8	16	88.9	747	10	CL169941
9	16	88.9	752	10	CW385975
10	16	88.9	759	2	BG89203
11	16	88.9	761	10	CL169940
12	16	88.9	1030	10	CL033121
13	15	83.3	85	6	CD963839
14	15	83.3	95	10	CG560188
15	15	83.3	102	10	CG671007
16	15	83.3	208	7	CO323095
17	15	83.3	238	10	CG556891
18	15	83.3	247	8	CX626914
19	15	83.3	285	3	BI491822
20	15	83.3	306	2	BF353376
21	15	83.3	308	2	BG184004
22	15	83.3	336	2	BG790049

C 23	15	83.3	345	3	BM443576	BM443576
C 24	15	83.3	346	2	BB710886	BB710886
C 25	15	83.3	348	5	BU019684	BU019684
C 26	15	83.3	365	7	CO190893	CO190893
C 27	15	83.3	374	1	AW020862	AW020862
C 28	15	83.3	401	10	AB082236	AB082236
C 29	15	83.3	405	9	BH388002	BH388002
C 30	15	83.3	435	2	BG181938	BG181938
C 31	15	83.3	437	1	AW317773	AW317773
C 32	15	83.3	441	2	BG187151	BG187151
C 33	15	83.3	444	5	BQ977181	BQ977181
C 34	15	83.3	445	6	CA938690	CA938690
C 35	15	83.3	446	5	BU761255	BU761255
C 36	15	83.3	449	9	AO631994	AO631994
C 37	15	83.3	452	2	BG205213	BG205213
C 38	15	83.3	465	2	BI071352	BI071352
C 39	15	83.3	471	2	BG187152	BG187152
C 40	15	83.3	476	1	AW099240	AW099240
C 41	15	83.3	496	8	DN650903	DN650903
C 42	15	83.3	501	2	BG214697	BG214697
C 43	15	83.3	511	1	AI150588	AI150588
C 44	15	83.3	516	1	AL900125	AL900125
C 45	15	83.3	533	8	DN650904	DN650904

## ALIGNMENTS

### RESULT 1

AJ641058/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 2

BE153987

LOCUS

AJ641058 794 bp mRNA linear EST 28-JAN-2005  
AJ641058 Populus tremula x P. tremuloides/Amanita muscaria mixed  
EST library Populus tremula x P. tremuloides/Amanita muscaria mixed  
EST library cDNA clone ptamabc210068e03, mRNA sequence.

ACCESSION AJ641058 GI:58309785  
VERSION AJ641058.1  
KEYWORDS Populus tremula x P. tremuloides/Amanita muscaria mixed EST library  
SOURCE Populus tremula x P. tremuloides/Amanita muscaria mixed EST library  
ORGANISM Eukaryota; mixed EST libraries.  
REFERENCE 1 (bases 1 to 794)  
AUTHORS Bekel, T., Meyer, F., Kuester, H., Manthey, K., Perlick, A., Puehler, A., Bock, A. and Nehls, U.  
TITLE ESTs of fully developed ectomycorrhizas formed between Populus tremula x tremuloides and Amanita muscaria  
JOURNAL Unpublished (2005)  
COMMENT Contact: Bekel T.  
Physiologische Oekologie der Pflanzen  
Eberhard-Karls-Universitaet  
Auf der Morgenstelle 1, Tuebingen, BW 72076, Germany.

FEATURES  
source 1..794  
/organism="Populus tremula x P. tremuloides/Amanita muscaria mixed EST library"  
/mol\_type="mRNA"  
/db\_xref="taxon:1433775"  
/clone="ptamabc210068e03"  
/clone\_lib="Populus tremula x P. tremuloides/Amanita muscaria mixed EST library"

ORIGIN  
Query Match 94.4%; Score 17; DB 1; Length 794;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCAGGGCCATAATTAT 18

Db 469 AGCAGGGCCATAATTAT 453

RESULT 2

BE153987

LOCUS

BE153987

312 bp mRNA linear EST 21-JUN-2000

```

DEFINITION PMO-HT0339-060400-009-C04 HT0339 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE153987
VERSION BE153987.1 GI:8616617
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 312)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asmpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=6t2=PMO-HT0339-060400-009-C04&t3=2000-04-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 226.
Location/Qualifiers
1..312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0339"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCAGGGCCCAATTAT 18
Db 274 GCAGGGCCCAATTAT 289

RESULT 3
LOCUS BI432519 340 bp mRNA linear EST 30-APR-2003
DEFINITION EST535280 P. infestans-challenged potato leaf, compatible reaction
Solanum tuberosum cDNA clone PPCAR82 5' sequence, mRNA sequence.
ACCESSION BI432519
VERSION BI432519.1 GI:15257209
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.

PMO-HT0339-060400-009-C04 HT0339 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE153987
VERSION BE153987.1 GI:8616617
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 312)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asmpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=6t2=PMO-HT0339-060400-009-C04&t3=2000-04-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 226.
Location/Qualifiers
1..312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0339"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCAGGGCCCAATTAT 18
Db 274 GCAGGGCCCAATTAT 289

RESULT 3
LOCUS BI432519 340 bp mRNA linear EST 30-APR-2003
DEFINITION EST535280 P. infestans-challenged potato leaf, compatible reaction
Solanum tuberosum cDNA clone PPCAR82 5' sequence, mRNA sequence.
ACCESSION BI432519
VERSION BI432519.1 GI:15257209
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.

```

```

REFERENCE 1 (bases 1 to 340)
AUTHORS Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Roming,C.M., Fry,W.E. and Baker,B.
TITLE Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
JOURNAL Unpublished (2000)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13P-R
Location/Qualifiers
1..340
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCAR82"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf, compatible reaction"
/notes="Vector: p Bluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Corneil University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."

ORIGIN
Query Match 88.9%; Score 16; DB 3; Length 340;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCCAATT 16
Db 268 GAGCAGGGCCCAATT 283

RESULT 4
LOCUS T14826 439 bp mRNA linear EST 28-JUL-1995
DEFINITION crs268 lambdaZAPST Ricinus communis cDNA clone pcrs268, mRNA sequence.
ACCESSION T14826
VERSION T14826.1 GI:688463
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae; Ricinus.
REFERENCE 1 (bases 1 to 439)
AUTHORS vandewoo,F.J., Turner,S. and Somerville,C.
TITLE Expressed sequence tags from developing castor seeds
JOURNAL Plant Physiol. 108, 1141-1150 (1995)
COMMENT Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3.
Location/Qualifiers

```

```

source
1. .439
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcrs268"
/clone_lib="lambdazapst"
/note="Vector: lambdazapII; Site 1: EcoRI; Site 2: XhoI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdazapII according
to the instructions of the manufacturer (Stratagene):
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate. "

ORIGIN
Query Match      88.9%; Score 16; DB 8; Length 439;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATT 16
|||||
Db 317 GAGCAGGGCCATAATT 332

RESULT 5
BP191026/c
LOCUS      500 bp      mRNA      linear      EST 17-JUL-2003
DEFINITION      BP191026 planarian head cDNA Dugesia japonica cDNA clone 06171_HH,
mRNA sequence.
ACCESSION      BP191026
VERSION
KEYWORDS
SOURCE
ORGANISM      Dugesia japonica
Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata;
Tricladida; Paludicola; Dugesidae; Dugesia.
1 (bases 1 to 500)
Mineta,K., Nakazawa,M., Cebria,F., Ikeo,K., Agata,K. and
Gojobori,T.
Origin and evolutionary process of the CNS elucidated by
comparative genomics analysis of planarian ESTs
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7666-7671 (2003)
12802012
Contact: Katsuhiko Mineta
National Institute of Genetics, Center for Information Biology and
DNA Data Bank of Japan
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6847
Fax: 81-559-81-6848
Email: kmineta@lab.nig.ac.jp
These clones and additional information are obtained from our web
site: http://www.cib.nig.ac.jp/dda/.

FEATURES
source
1. .500
/organism="Dugesia japonica"
/mol_type="mRNA"
/db_xref="taxon:6161"
/clone="06171_HH"
/tissue_type="head"
/dev_stage="adult"
/clone_lib="Planarian head cDNA"

ORIGIN
Query Match      88.9%; Score 16; DB 3; Length 500;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCAGGGCCATAATTA 17
|||||

Db
368 ACCAGGGCCATAATTA 353

RESULT 6
BG600462
LOCUS      652 bp      mRNA      linear      EST 07-MAR-2003
DEFINITION      EST505357 cSTS Solanum tuberosum cDNA clone CSTS2911 5' sequence,
mRNA sequence.
ACCESSION      BG600462
VERSION
KEYWORDS
SOURCE
ORGANISM      Solanum tuberosum (potato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 652)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Romning,C., Tanksley,S. and Baker,B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.

FEATURES
source
1. .652
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="CSTS2911"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone_lib="cSTS"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATT 16
|||||
Db 521 GAGCAGGGCCATAATT 536

RESULT 7
CX409188
LOCUS      740 bp      mRNA      linear      EST 06-JAN-2005
DEFINITION      JGI XZT32096.fwd NIH XGC tropTad5 Xenopus tropicalis cDNA clone
IMAGE:7608418 5', mRNA sequence.
ACCESSION      CX409188
VERSION
KEYWORDS
SOURCE
ORGANISM      Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 740)
Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.

```

**TITLE**  
JOURNAL  
COMMENT

DOE Joint Genome Institute Xenopus tropicalis EST project  
 Unpublished (2004)  
 Contact: Lindquist, E.A., Richardson, P.  
 DOE Joint Genome Institute  
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 Tel: 925 296 5600  
 Fax: 925 296 5710  
 Email: cdna@jgi-psf.org

Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>  
 cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley  
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>  
 Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
<http://image.llnl.gov>

Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
 Plate: XZT 0333 row: o column: 8  
 High quality sequence stop: 706.  
 Location/Qualifiers  
 1. .740  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:8364"  
 /clone="IMAGE:7608418"  
 /tissue\_type="whole embryo"  
 /dev\_stage="Tadpole (st. 36-41)"  
 /lab\_host="E. coli XL1-Blue derivative, Stratagene Electropen-Blue"  
 /clone\_lib="NIH XGC tropTads"  
 /note="Vector: PCS108; Site\_1: SalI; Site\_2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108  
 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"

**FEATURES**  
source

Query Match 88.9%; Score 16; DB 8; Length 740;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 3 GCAGGGCCCAATTAT 18  
 |||||  
**Db** 28 GCAGGGCCCAATTAT 43

**RESULT 8**  
 CL169941/c 747 bp DNA linear GSS 06-JAN-2004  
**LOCUS** 104.370 10813405.148 31788.109 Sorghum methylation-filtered library  
**DEFINITION** (LibID\_104) Sorghum bicolor genomic clone 10813405, genomic survey sequence.  
 CL169941  
 CL169941.1 GI:40682353  
**VERSION** GSS.  
**KEYWORDS** Sorghum bicolor (sorghum)  
**SOURCE** Sorghum bicolor  
**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 747)  
**REFERENCE** Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Hootman, H., Roe, B.A., Wiley, G., Korfi, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Martienssen, R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)

**TITLE**  
JOURNAL

**TITLE**  
JOURNAL  
COMMENT

15660154  
 Contact: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: 370 row: e column: 13  
 Seq primer: SWfor Forward  
 Class: methylation filtered  
 High quality sequence stop: 747.  
 Location/Qualifiers  
 1. .747  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:4558"  
 /clones="10813405"  
 /clone\_lib="Sorghum methylation-filtered library (LibID: 104)"  
 /note="Organ: leaf; Vector: pBCSK(-); Site\_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."

**FEATURES**  
source

Query Match 88.9%; Score 16; DB 10; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 2 AGCAGGGCCCAATTA 17  
 |||||  
**Db** 402 AGCAGGGCCCAATTA 387

**RESULT 9**  
 CW385975 752 bp DNA linear GSS 01-NOV-2004  
**LOCUS** fbb001f069k13k0 Sorghum methylation filtered library (LibID: 104)  
**DEFINITION** Sorghum bicolor genomic clone fbb001f069k13, genomic survey sequence.  
 CW385975  
 CW385975.1 GI:55104419  
**VERSION** GSS.  
**KEYWORDS** Sorghum bicolor (sorghum)  
**SOURCE** Sorghum bicolor  
**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 752)  
**REFERENCE** Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Hootman, H., Roe, B.A., Wiley, G., Korfi, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Martienssen, R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
 15660154  
**TITLE** CL169941  
**JOURNAL** CL169941.1 GI:40682353  
**COMMENT** GSS.  
 Sorghum bicolor (sorghum)  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: fbb001f069 row: k column: 13  
 Seq primer: k Reverse  
 Class: methylation filtered  
 High quality sequence stop: 752.  
 Location/Qualifiers  
 1. .752  
 /organism="Sorghum bicolor"

/mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone="f06b001f069k13"  
 /clone\_lib="Sorghum methylation filtered library (LibID: 104)"  
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

## ORIGIN

Query Match 88.9%; Score 16; DB 10; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGGGCCATAATTA 17

Db 599 AGCAGGGCCATAATTA 614

## RESULT 10

BG889203

LOCUS

DEFINITION EST515054 cSTD Solanum tuberosum cDNA clone cSTD13G2 5' sequence,  
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 759)

AUTHORS

van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A.,  
 Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

TITLE

JOURNAL

COMMENT

The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@igr.org  
 This clone can be obtained from the University of Arizona Genomics  
 Institute. Orders can be made through URL:  
 http://genome.arizona.edu/orders/  
 Seq primer: M13F-R.

## FEATURES

source

1..759

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="cSTD13G2"

/tissue\_type="dormant tuber"

/dev\_stage="one month post-harvest"

/lab\_host="SOLR"

/clone\_lib="cSTD"

/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; This library targets genes expressed in dormant  
 tubers. This library was made from sections of dormant  
 tubers, avoiding the buds and epidermis. Tubers were stored  
 for one month post-harvest at 40C. The tuber was peeled,  
 well away from the surface. Then it was chopped into 1-2  
 mm cubes and immediately frozen in liquid nitrogen. This  
 library is noted as P4 in Tanksley lab notebooks."

## ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 759;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCATAATT 16

Db 606 GAGCAGGGCCATAATT 621

## RESULT 11

CU169940

LOCUS

DEFINITION

CL169940 761 bp DNA linear GSS 06-JAN-2004  
 104 370 10813405 116 31789 109 Sorghum methylation-filtered library  
 (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey  
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 761)

AUTHORS

Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,  
 Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,  
 McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,  
 Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddaloeh,J.A. and  
 Martienssen,R.A.

TITLE

JOURNAL

PUBMED

COMMENT

Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)

CONTACT: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@origenomics.com

Plate: 370 row: e column: 13

Seq primer: T3 Reverse

Class: methylation filtered

High quality sequence stop: 761.

Location/Qualifiers

1..761

/organism="Sorghum bicolor"

/mol\_type="genomic DNA"

/cultivar="ATx623"

/db\_xref="taxon:4558"

/clone="10813405"

/clone\_lib="Sorghum methylation-filtered library (LibID: 104)"

/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA  
 prepared from purified nuclei was randomly sheared,  
 end-repaired, size fractionated to enrich for the 0.5 to 5  
 kb fraction, ligated into HincII-digested pBCSK(-) vector  
 and electroporated into E. coli cells. This is a  
 methylation-filtered library."

## ORIGIN

Query Match 88.9%;

Best Local Similarity 100.0%;

Matches 16; Conservative 0;

Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGGGCCATAATTA 17

Db 639 AGCAGGGCCATAATTA 654

## RESULT 12

CU033121/c

LOCUS

DEFINITION

CU033121 1030 bp DNA linear GSS 31-DEC-2003  
 CH216-36A12 Sp6.1 CH216 Xenopus tropicalis genomic clone  
 CH216-36A12, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

CU033121.1 GI:40483484

GSS.

SOURCE  
ORGANISM  
Xenopus tropicalis (western clawed frog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
REFERENCE  
1 (bases 1 to 1030)  
AUTHORS  
Krenitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
Mardis, E. and Wilson, R.  
TITLE  
A physical map of the xenopus tropicalis genome  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Richard K Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 175000 Std Error: 0.00  
Seq primer: Sp6 ATTAGGTGACACTATAG  
Classes: BAC ends  
High quality sequence start: 29  
High quality sequence stop: 943.  
FEATURES  
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1..1030  
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/mol\_type="genomic DNA"  
/strain="Nigerian frog"  
/db\_xref="taxon:8364"  
/clone="CH216-36A12"  
/sex="male"  
/cell\_line="Stock 248 F7A2, inbred N7"  
/clone\_lib="CH216"  
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis  
BAC library"  
ORIGIN  
Query Match 88.9%; Score 16; DB 10; Length 1030;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 GCAGGGCCATAATTAT 18  
Db 47 GCAGGGCCATAATTAT 32  
RESULT 13  
CD963839/c  
LOCUS  
CD963839  
DEFINITION  
SDY 133 GeneTag2 Zea mays cdna, mRNA sequence.  
ACCESSION  
CD963839  
VERSION  
EST.  
KEYWORDS  
Zea mays  
SOURCE  
Zea mays  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 85)  
AUTHORS  
Genoplante.  
TITLE  
Genoplante, a major partnership french program in plant genomics  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).  
FEATURES  
source  
1..85  
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/cultivar="mixture"  
/db\_xref="taxon:4577"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGCAGGGCCATAAT 15  
Db 61 GAGCAGGGCCATAAT 47  
RESULT 14  
CG560188  
LOCUS  
CG560188  
DEFINITION  
OST180267 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST180267,  
mRNA sequence.  
ACCESSION  
CG560188  
VERSION  
GSS.  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
Mus musculus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 95)  
AUTHORS  
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., Beltrandeirio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W. Jr., Kipp, P., Kohlauf, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Perren, C. and Sands, A.T.  
TITLE  
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED  
14610273  
COMMENT  
Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
FEATURES  
source  
1..95  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST180267"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"  
ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 GCAGGGCCATAATTA 17  
Db 37 GCAGGGCCATAATTA 51  
RESULT 15  
CG671007  
LOCUS  
CG671007  
DEFINITION  
OST472166 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST472166,  
mRNA sequence.  
ACCESSION  
CG671007  
VERSION  
GSS.  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE

us-10-018-716b-1.Oligo.rst

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 102)
REFERENCE
AUTHORS
Zambrowicz B.P., Abulin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W., Jr., Kipp,P.P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Shwartz,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
TITLE
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL
PUBMED
14610273
COMMENT
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1..102
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/db_xref="taxon:10090"
/clone="OST472166"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCAGGGCCATAATTA 17
|||||
DB 28 GCAGGGCCATAATTA 42
Search completed: November 30, 2005, 00:44:45
Job time : 1871.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:31 ; Search time 136.5 Seconds  
(without alignments)  
19.597 Million cell updates/sec

Title: US-10-018-716B-1

Perfect score: 18

Sequence: 1 gagcaggccataattat 18

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 3205263 seqs, 74304013 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_NA\_New.\*  
1: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	77.8	1149	US-11-082-389-213	Sequence 213, App
C 2	12	66.7	19	US-11-101-244-173294	Sequence 173294,
C 3	12	66.7	19	US-11-101-244-339765	Sequence 339765,
C 4	12	66.7	19	US-11-101-244-600029	Sequence 600029,
C 5	12	66.7	19	US-11-101-244-1044082	Sequence 1044082,
C 6	12	66.7	19	US-11-101-244-1044118	Sequence 1044118,
C 7	12	66.7	19	US-11-101-244-1152178	Sequence 1152178,
C 8	12	66.7	19	US-11-101-244-1152276	Sequence 1152276,
C 9	12	66.7	19	US-11-101-244-1311535	Sequence 1311535,
C 10	12	66.7	19	US-11-101-244-1430673	Sequence 1430673,
C 11	12	66.7	19	US-11-101-244-1430674	Sequence 1430674,
C 12	12	66.7	19	US-11-083-784-173294	Sequence 173294,
C 13	12	66.7	19	US-11-083-784-339765	Sequence 339765,
C 14	12	66.7	19	US-11-083-784-600029	Sequence 600029,
C 15	12	66.7	19	US-11-083-784-1044082	Sequence 1044082,
C 16	12	66.7	19	US-11-083-784-1044118	Sequence 1044118,
C 17	12	66.7	19	US-11-083-784-1152178	Sequence 1152178,
C 18	12	66.7	19	US-11-083-784-1152276	Sequence 1152276,
C 19	12	66.7	19	US-11-083-784-1311535	Sequence 1311535,
C 20	12	66.7	19	US-11-083-784-1430673	Sequence 1430673,
C 21	12	66.7	19	US-11-083-784-1430674	Sequence 1430674,
C 22	12	66.7	844	US-11-082-389-441	Sequence 441, App
C 23	12	66.7	1095	US-11-082-389-439	Sequence 439, App

C 24	12	66.7	1656	1	US-10-131-826A-239	Sequence 239, App
C 25	12	66.7	3458	1	US-10-793-626-3510	Sequence 3510, App
C 26	12	66.7	6708	1	US-10-821-234-164	Sequence 164, App
C 27	12	66.7	7382	1	US-10-839-211-1	Sequence 1, Appli
C 28	11	61.1	19	8	US-11-101-244-341877	Sequence 341877,
C 29	11	61.1	19	8	US-11-101-244-343613	Sequence 343613,
C 30	11	61.1	19	8	US-11-101-244-343631	Sequence 343631,
C 31	11	61.1	19	8	US-11-101-244-374101	Sequence 374101,
C 32	11	61.1	19	8	US-11-101-244-380293	Sequence 380293,
C 33	11	61.1	19	8	US-11-101-244-425500	Sequence 425500,
C 34	11	61.1	19	8	US-11-101-244-425510	Sequence 425510,
C 35	11	61.1	19	8	US-11-101-244-425572	Sequence 425572,
C 36	11	61.1	19	8	US-11-101-244-661639	Sequence 661639,
C 37	11	61.1	19	8	US-11-101-244-661697	Sequence 661697,
C 38	11	61.1	19	8	US-11-101-244-716963	Sequence 716963,
C 39	11	61.1	19	8	US-11-101-244-716974	Sequence 716974,
C 40	11	61.1	19	8	US-11-101-244-725866	Sequence 725866,
C 41	11	61.1	19	8	US-11-101-244-764763	Sequence 764763,
C 42	11	61.1	19	8	US-11-101-244-764784	Sequence 764784,
C 43	11	61.1	19	8	US-11-101-244-764830	Sequence 764830,
C 44	11	61.1	19	8	US-11-101-244-799257	Sequence 799257,
C 45	11	61.1	19	8	US-11-101-244-828288	Sequence 828288,

ALIGNMENTS

RESULT 1  
US-11-082-389-213/C  
; Sequence 213, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; TITLE OF INVENTION: TRANSPORT  
; FILE REFERENCE: BGI-131CPGN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 213  
; LENGTH: 1149  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1126)  
; OTHER INFORMATION: RXN00523

## US-11-082-389-213

Query Match 77.8%; Score 14; DB 9; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCATAA 14  
|||||  
Db 242 GAGCAGGGCCATAA 229

## RESULT 2

US-11-101-244-173294/c  
; Sequence 173294, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 173294  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-11-101-244-173294

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGGGCCATA 13  
|||||  
Db 14 AGCAGGGCCATA 3

## RESULT 3

US-11-101-244-339765  
; Sequence 339765, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 339765  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-11-101-244-339765

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCCATAATTA 17  
|||||  
Db 8 GGGCCAAUAUA 19

## RESULT 4

US-11-101-244-600029/c  
; Sequence 600029, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 600029  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-11-101-244-600029

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
|||||  
Db 14 GAGCAGGGCCAT 3

## RESULT 5

US-11-101-244-1044082/c  
; Sequence 1044082, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1044082  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-11-101-244-1044082

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
|||||  
DB 14 GAGCAGGGCCAT 3

## RESULT 6

US-11-101-244-1044118/c  
; Sequence 1044118, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1044118  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1044118

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
|||||  
DB 16 GAGCAGGGCCAT 5

## RESULT 7

US-11-101-244-1152178/c  
; Sequence 1152178, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1152178  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1152178

Query Match 66.7%; Score 12; DB 8; Length 19;

Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
|||||  
DB 16 GAGCAGGGCCAT 5

## RESULT 8

US-11-101-244-1152276/c  
; Sequence 1152276, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1152276  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1152276

## Query Match

Best Local Similarity 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
|||||  
DB 16 GAGCAGGGCCAT 5

## RESULT 9

US-11-101-244-1311535/c  
; Sequence 1311535, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1311535  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1311535

## Query Match

Best Local Similarity 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GGCCATAATTAT 18  
|||||  
Db 14 GGCCATAATTAT 3

RESULT 10  
US-11-101-244-1430673  
; Sequence 1430673, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1430673  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1430673

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 91.7%; Pred. No. 34;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
|||||  
Db 1 GAGCAGGGCCAU 12

RESULT 11  
US-11-101-244-1430674  
; Sequence 1430674, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1430674  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1430674

Query Match 66.7%; Score 12; DB 8; Length 19;  
Best Local Similarity 91.7%; Pred. No. 34;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
|||||  
Db 4 GAGCAGGGCCAU 15

RESULT 12  
US-11-083-784-173294/c  
; Sequence 173294, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 173294  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-173294

Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGGGCCATA 13  
|||||  
Db 14 AGCAGGGCCATA 3

RESULT 13  
US-11-083-784-339765  
; Sequence 339765, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 339765  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-339765

Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCCATAATTA 17  
Db 8 GGGCCAUAUAU 19

RESULT 14

US-11-083-784-600029/c  
; Sequence 600029, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 600029  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-600029

Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
Db 14 GAGCAGGGCCAT 3

RESULT 15

US-11-083-784-1044082/c  
; Sequence 1044082, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1044082  
; LENGTH: 19  
; TYPE: RNA

; ORGANISM: Homo sapiens  
US-11-083-784-1044082

Query Match 66.7%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCAT 12  
Db 14 GAGCAGGGCCAT 3

Search completed: November 29, 2005, 18:29:39  
Job time : 137.5 secs

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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:35 ; Search time 403.5 Seconds  
(without alignments)  
368.894 Million cell updates/sec

Title: US-10-018-716B-1

Perfect score: 18  
Sequence: 1 gacgaggccataattat 18

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main:  
1: /cgn2\_6/prodata/1/pubpna/us07\_PUBCOMB.seq.\*  
2: /cgn2\_6/prodata/1/pubpna/us08\_PUBCOMB.seq.\*  
3: /cgn2\_6/prodata/1/pubpna/us09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/prodata/1/pubpna/us09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/prodata/1/pubpna/us10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/prodata/1/pubpna/us10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/prodata/1/pubpna/us10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/prodata/1/pubpna/us10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/prodata/1/pubpna/us10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/prodata/1/pubpna/us11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	441	4	US-09-925-065A-192589
C 2	18	100.0	441	4	US-09-925-065A-192590
C 3	18	100.0	1922	8	US-10-349-528-4
C 4	18	100.0	2019	7	US-10-382-248-9
C 5	18	100.0	2393	5	US-10-225-567A-121
C 6	18	100.0	2393	5	US-10-207-655-64
C 7	18	100.0	2393	6	US-10-305-720-1209
C 8	16	88.9	201	8	US-10-719-993-38475
C 9	16	88.9	612	4	US-09-925-065A-391076
C 10	16	88.9	261638	8	US-10-719-993-6882
C 11	15	83.3	461	4	US-09-925-065A-328046
C 12	15	83.3	507	6	US-10-172-118-2085
C 13	15	83.3	507	7	US-10-342-887-2085
C 14	15	83.3	533	4	US-09-925-065A-520324
C 15	15	83.3	544	4	US-09-925-065A-539398
C 16	15	83.3	612	5	US-10-007-280A-106
C 17	15	83.3	628	5	US-10-007-280A-107
C 18	15	83.3	842	5	US-10-027-632-160723
C 19	15	83.3	842	5	US-10-027-632-160724
C 20	15	83.3	842	6	US-10-027-632-160723
C 21	15	83.3	842	6	US-10-027-632-160724
C 22	15	83.3	1634	7	US-10-424-599-84619
C 23	15	83.3	2021	8	US-10-739-930-4619

C 24	15	83.3	3659	10	US-11-097-143-15251	Sequence 15251, A
C 25	15	83.3	9140	10	US-11-097-143-15250	Sequence 15250, A
C 26	15	83.3	76829	9	US-10-737-082-27	Sequence 27, Appl
C 27	15	83.3	76829	7	US-10-765-790-27	Sequence 27, Appl
C 28	15	83.3	180227	7	US-10-322-281-308	Sequence 308, App
C 29	15	83.3	202251	5	US-10-087-192-985	Sequence 985, App
C 30	15	83.3	325348	6	US-10-085-117-358	Sequence 358, App
C 31	14	77.8	219	7	US-10-719-900-825663	Sequence 825663, A
C 32	14	77.8	285	8	US-10-437-963-7570	Sequence 7570, App
C 33	14	77.8	465	4	US-09-925-065A-622260	Sequence 95091, A
C 34	14	77.8	465	4	US-09-925-065A-622261	Sequence 622260, A
C 35	14	77.8	465	4	US-09-925-065A-622262	Sequence 622261, A
C 36	14	77.8	574	5	US-10-066-543-3296	Sequence 622262, A
C 37	14	77.8	591	5	US-10-027-632-15415	Sequence 3296, App
C 38	14	77.8	591	5	US-10-027-632-15415	Sequence 15415, A
C 39	14	77.8	591	5	US-10-027-632-15415	Sequence 15416, A
C 40	14	77.8	591	6	US-10-027-632-15416	Sequence 15415, A
C 41	14	77.8	600	4	US-09-925-065A-895996	Sequence 15416, A
C 42	14	77.8	611	5	US-10-027-632-224562	Sequence 895996, A
C 43	14	77.8	611	6	US-10-027-632-224562	Sequence 224562, A
C 44	14	77.8	668	7	US-10-437-963-3301	Sequence 224562, A
C 45	14	77.8	668	7	US-10-437-963-3301	Sequence 3301, App

ALIGNMENTS

RESULT 1  
US-09-925-065A-192589/c  
; Sequence 192589, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192589  
; LENGTH: 441  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-192589

Query Match 100.0%; Score 18; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;

QY 1 GAGCAGGGCCATAATTAT 18  
|||  
Db 335 GAGCAGGGCCATAATTAT 318

RESULT 2  
US-09-925-065A-192590/c  
; Sequence 192590, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192590  
; LENGTH: 441  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-192590

Query Match 100.0%; Score 18; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18  
Db 335 GAGCAGGGCCATAATTAT 318

RESULT 3  
US-10-349-528-4/c  
; Sequence 4, Application US/10349528  
; Publication No. US20040253668A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMANATHAN, Chandra  
; APPLICANT: GOPAL, Shuba  
; APPLICANT: MINTIER, Gabe  
; APPLICANT: FEDER, John  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF  
; FILE REFERENCE: D0210  
; CURRENT APPLICATION NUMBER: US/10/349,528  
; CURRENT FILING DATE: 2003-01-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 4  
; LENGTH: 1922  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-10-349-528-4

Query Match 100.0%; Score 18; DB 8; Length 1922;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18  
Db 28 GAGCAGGGCCATAATTAT 11

RESULT 4  
US-10-382-248-9/c  
; Sequence 9, Application US/10382248  
; Publication No. US20040058347A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook, et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-568C  
; CURRENT APPLICATION NUMBER: US/10/382,248  
; CURRENT FILING DATE: 2003-03-05  
; PRIOR APPLICATION NUMBER: 60/366,928  
; PRIOR FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: 60/361,974  
; PRIOR FILING DATE: 2002-03-06  
; PRIOR APPLICATION NUMBER: 60/365,477  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 60/401,661  
; PRIOR FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 9  
; LENGTH: 2019  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (61)..(1959)  
US-10-382-248-9

Query Match 100.0%; Score 18; DB 7; Length 2019;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18  
Db 72 GAGCAGGGCCATAATTAT 55

RESULT 5  
US-10-225-567A-121/c  
; Sequence 121, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 121  
; LENGTH: 2393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-121

Query Match 100.0%; Score 18; DB 5; Length 2393;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18  
Db 78 GAGCAGGGCCATAATTAT 61

RESULT 6  
US-10-207-655-64/c  
; Sequence 64, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 64  
; LENGTH: 2393



```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-64

Query Match      100.0%; Score 18; DB 5; Length 2393;
Best Local Similarity 100.0%; Pred. No. 0.48; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 GAGCAGGGCCATAATTAT 18
   ||||||||||||||||
Db 78 GAGCAGGGCCATAATTAT 61

RESULT 7
US-10-305-720-1209/c
; Sequence 1209, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1209
; LENGTH: 2393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 GI82770
US-10-305-720-1209

Query Match      100.0%; Score 18; DB 6; Length 2393;
Best Local Similarity 100.0%; Pred. No. 0.48; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 GAGCAGGGCCATAATTAT 18
   ||||||||||||||||
Db 78 GAGCAGGGCCATAATTAT 61

RESULT 8
US-10-719-993-38475/c
; Sequence 38475, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38475
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-38475

Query Match      88.9%; Score 16; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 7.7; 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 3 GCAGGGCCATAATTAT 18
   ||||||||||||||||
Db 128 GCAGGGCCATAATTAT 113
```

```
RESULT 9
US-09-925-065A-391076/c
; Sequence 391076, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391076
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-391076

Query Match      88.9%; Score 16; DB 4; Length 612;
Best Local Similarity 100.0%; Pred. No. 7.8; 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2 AGCAGGGCCATAATTAT 17
   ||||||||||||||||
Db 580 AGCAGGGCCATAATTAT 565

RESULT 10
US-10-719-993-6882/c
; Sequence 6882, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6882
; LENGTH: 261638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6882

Query Match      88.9%; Score 16; DB 8; Length 261638;
Best Local Similarity 100.0%; Pred. No. 8.4; 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 3 GCAGGGCCATAATTAT 18
   ||||||||||||||||
Db 29154 GCAGGGCCATAATTAT 29139

RESULT 11
US-09-925-065A-328046/c
; Sequence 328046, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

```
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328046
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-328046
```

```
Query Match      83.3%; Score 15; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 AGCAGGGCCATAATT 16
Db      25 AGCAGGGCCATAATT 11
      |||||
```

## RESULT 12

```
US-10-172-118-2085
; Sequence 2085, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberte, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Contig23454
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2085
```

```
Query Match      83.3%; Score 15; DB 6; Length 507;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 AGCAGGGCCATAATT 16
Db      163 AGCAGGGCCATAATT 177
      |||||
```

## RESULT 13

```
US-10-342-887-2085
; Sequence 2085, Application US/10342887
; Publication No. US20040058340A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberte, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-2085
```

```
Query Match      83.3%; Score 15; DB 7; Length 507;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 AGCAGGGCCATAATT 16
Db      163 AGCAGGGCCATAATT 177
      |||||
```

## RESULT 14

```
US-09-925-065A-520324
; Sequence 520324, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 520324
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-520324
```

```
Query Match      83.3%; Score 15; DB 4; Length 533;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 AGCAGGGCCATAATT 16
Db      354 AGCAGGGCCATAATT 368
      |||||
```

```
RESULT 15
US-09-925-065A-539398
; Sequence 539398, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 539398
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539398
```

```
Query Match      83.3%; Score 15; DB 4; Length 544;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2 AGCAGGGCCATAATT 16
Db      354 AGCAGGGCCATAATT 368
```

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Search completed: November 29, 2005, 20:39:06
Job time : 404.5 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:25:08 ; Search time 894.5 Seconds  
(without alignments)  
1143.859 Million cell updates/sec

Title: US-10-018-716B-1  
Perfect score: 18  
Sequence: 1 gagcaggccataattat 18

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- GenEmbl:\*  
1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_scs.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	856	8 HSFSTHR	X68044 H.sapiens m
C 2	18	100.0	1724	8 S73199	S73199 follicle-st
C 3	18	100.0	1734	8 HSFSHX1	Z34260 H.sapiens D
C 4	18	100.0	2179	6 AR003719	AR003719 Sequence
C 5	18	100.0	2179	6 AR067576	AR067576 Sequence
C 6	18	100.0	2179	6 AR207283	AR207283 Sequence
C 7	18	100.0	2179	8 S59900	S59900 follicle st
C 8	18	100.0	2186	8 HUMSHREC	M95489 H.sapiens f
C 9	18	100.0	2222	6 A76125	A76125 Sequence 1
C 10	18	100.0	2374	6 CQ715054	CQ715054 Sequence
C 11	18	100.0	2393	6 AR270646	AR270646 Sequence
C 12	18	100.0	2393	6 AX548836	AX548836 Sequence
C 13	18	100.0	2393	8 HUMFSHRE	M65085 Human folli
C 14	18	100.0	121688	8 AC092533	AC092533 Homo sapi
C 15	18	100.0	158709	14 AC083827	AC083827 Homo sapi
C 16	17	94.4	162	8 HSFSHX1	X91738 H.sapiens g
C 17	16	88.9	1041	5 AY625217	AY625217 Priotelus
C 18	16	88.9	95681	8 AL157890	AL157890 Human DNA

C 19	88.9	113657	14	AC166226	AC166226	Sorex ara
C 20	88.9	121589	14	AC137655	AC137655	Bos tauru
C 21	88.9	125311	8	AC068758	AC068758	Homo sapi
C 22	88.9	127015	14	AC151504	AC151504	Dasyvus n
C 23	88.9	160179	14	AC092930	AC092930	Homo sapi
C 24	88.9	168380	8	AC063933	AC063933	Homo sapi
C 25	88.9	169314	14	AC148413	AC148413	Callithri
C 26	88.9	169996	14	AC053521	AC053521	Homo sapi
C 27	88.9	171267	14	AC154087	AC154087	Alligator
C 28	88.9	171990	14	AC153783	AC153783	Rhinoloph
C 29	88.9	185798	14	AC158248	AC158248	Callithri
C 30	88.9	187465	9	AC132305	AC132305	Mus muscu
C 31	88.9	191709	9	AC115890	AC115890	Mus muscu
C 32	88.9	197909	9	AC158658	AC158658	Mus muscu
C 33	88.9	198551	9	AC068605	AC068605	Mus muscu
C 34	88.9	210236	14	AC115069	AC115069	Bos tauru
C 35	88.9	236157	14	AC111356	AC111356	Rattus no
C 36	88.9	258499	14	AC130987	AC130987	Rattus no
C 37	88.9	283919	14	AC095169	AC095169	Rattus no
C 38	83.3	481	6	AR496706	AR496706	Sequence
C 39	83.3	481	6	AR511988	AR511988	Sequence
C 40	83.3	612	6	AX554759	AX554759	Sequence
C 41	83.3	628	6	AX554760	AX554760	Sequence
C 42	83.3	1303	5	CR760514	CR760514	Xenopus t
C 43	83.3	1437	5	BC061373	BC061373	Xenopus t
C 44	83.3	1727	15	AB023467	AB023467	Metschnik
C 45	83.3	2652	8	BC034230	BC034230	Homo sapi

ALIGNMENTS

RESULT 1  
HSFSTHR/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS

HSFSTHR 856 bp mRNA linear PRI 07-FEB-1993  
H.sapiens mRNA for follicle-stimulating hormone receptor.  
X68044.1 GI:31473  
follicle stimulating hormone receptor.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 856)  
Gromoll, J., Gudermann, T. and Nieschlag, E.  
Molecular cloning of a truncated isoform of the human follicle  
stimulating hormone receptor  
Biochem. Biophys. Res. Commun. 188 (3), 1077-1083 (1992)  
135989  
2  
Gromoll, J.  
Direct Submission  
Submitted (11-AUG-1992) J. Gromoll, Institut f  
Reproduktionsmedizin, Steinfurter Strasse 107, 4400 Muenster, FRG  
Location/Qualifiers  
1..856  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/feature\_type="testis"  
17..856  
/codon\_start=1  
/product="follicle stimulating hormone receptor"  
/protein\_id="CAA48179.1"  
/db\_xref="GI:31474"  
/db\_xref="GOA:P23945"  
/translation="MALILVSLAFRLGSGCHRHICHSNRFVLCQSKVTEIPSDL  
PRNALEFLVTKLVIOKAGSGFDLEKIEISONDVLEIVADVSNLPKLHEIRI  
EKANLLIYNPAFQNLNQLVLLISNTGKILHPDVHKHLSQKVLDDQDNINHTI  
ERNFVGLSFESVILWLNKQIOEIHNCAFNGLDDELNLNNNNLEELPNQVFGAS  
GPVILSELPICNKFIILQREVDTMTQTRGQRSLADBNSSYSYSGFDMTTFDYDLC

```

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 856;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
|||||
Db 28 GAGCAGGGCCATAATTAT 11

RESULT 2
S73199/c
LOCUS 1724 nt.
DEFINITION follicle-stimulating hormone receptor {5' region} [human, Genomic,
S73199
ACCESSION S73199
VERSION S73199.1 GI:685036
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1724)
AUTHORS Gromoll,J., Dankbar,B. and Gudermann,T.
TITLE Characterization of the 5' flanking region of the human
JOURNAL follicle-stimulating hormone receptor gene
PUBMED Mol. Cell. Endocrinol. 102 (1-2), 93-102 (1994)
7926278
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gbbseq 155309] from the original journal article.
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PRNAIETL"

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
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Db 1498 GAGCAGGGCCATAATTAT 1481

RESULT 3
HFSHX1/c
LOCUS 1734 bp
DEFINITION H.sapiens DNA for follicle stimulating hormone (FSH) receptor.
ACCESSION Z34260
VERSION Z34260.1 GI:1052701
KEYWORDS follicle stimulating hormone receptor; FSH-receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1734)

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AUTHORS Gromoll,J.
JOURNAL Thesis (1994) Institute of Reproductive Medicine, University of
Muenster
REFERENCE 2 (bases 1 to 1734)
AUTHORS Gromoll,J.
TITLE Characterization of the 5'-flanking region of the human follicle
stimulating hormone receptor gene
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1734)
AUTHORS Gromoll,J.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1994) Gromoll J., University of Muenster
Institute of Reproductive Medicine Steinfurter Str. 107 Muenster
Germany 48149
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
|||||
Db 1498 GAGCAGGGCCATAATTAT 1481

RESULT 4
AR003719/c
LOCUS 2179 bp
DEFINITION Sequence 1 from patent US 5744448.
ACCESSION AR003719
VERSION AR003719.1 GI:3964978
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2179)
AUTHORS Kelton,C. Ann., Cheng,S.Vui.Yen., Nugent,N.Patrice. and
Schweickhardt,R.Lynn.
TITLE Human follicle stimulating hormone receptor
JOURNAL Patent: US 5744448-A 1 28-APR-1998;
FEATURES Location/Qualifiers
source
1..2179
/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
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Db 86 GAGCAGGGCCATAATTAT 69

RESULT 5
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LOCUS 2179 bp
DEFINITION Sequence 1 from patent US 5851768.
ACCESSION AR067576

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	Sequence 1 from Patent WO9320199.			
ACCESSION	A76125			
	Version			
VERSION	A76125.1			
	GI:6088261			
KEYWORDS				
	Homo sapiens (human)			
SOURCE				
	Homo sapiens			
ORGANISM				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE				
	AUTHORS			
TITLE				
	HUMAN GONADOTROPIN RECEPTOR (FSH RECEPTOR)			
JOURNAL				
	Patent; WO 9320199-A 1 14-OCT-1993;			
FEATURES				
	AK20 NV (NL); DIJKEVA REIN (NL)			
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ACCESSION	A76125			
	Version			
VERSION	A76125.1			
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KEYWORDS				
	Homo sapiens (human)			
SOURCE				
	Homo sapiens			
ORGANISM				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE				
	AUTHORS			
TITLE				
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JOURNAL				
	Patent; WO 9320199-A 1 14-OCT-1993;			
FEATURES				
	AK20 NV (NL); DIJKEVA REIN (NL)			
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Db	96 GAGCAGGGCCATAATTAT 79			
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LOCUS	CQ715054			
	Sequence 988 from Patent WO02068579.			
ACCESSION	CQ715054			
	Version			
VERSION	CQ715054.1			
	GI:42275911			
KEYWORDS				
	Homo sapiens (human)			
SOURCE				
	Homo sapiens			
ORGANISM				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE				
	AUTHORS			
TITLE				
	Kits, such as nucleic acid arrays, comprising a majority of			
JOURNAL				
	humanexons or transcripts, for detecting expression and other uses			
FEATURES				
	thereof			
source				



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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 78 GAGCAGGGCCATAATTAT 61

RESULT 12
LOCUS AX548836 2393 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 121 from Patent WO02061087.
ACCESSION AX548836
VERSION AX548836.1 GI:25813727
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Burmer,G.C., Rough,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 121 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
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Location/Qualifiers
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ORIGIN
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGGCCATAATTAT 18
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Db 78 GAGCAGGGCCATAATTAT 61

HUMFSHRE 2393 bp mRNA linear PRI 12-JAN-2005
Human follicle stimulating hormone receptor mRNA, complete cds.
M65085
Version M65085.1 GI:182770
Keywords follicle stimulating hormone (FSH) receptor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 2393)
REFERENCE Minegishi,T., Nakamura,K., Takakura,Y., Ibuki,Y., Igarashi,M. and
AUTHORS Minegishi,T.
TITLE Cloning and sequencing of human FSH receptor cDNA
JOURNAL Biochem. Biophys. Res. Commun. 175 (3), 1125-1130 (1991)
PUBMED 1709010
COMMENT Original source text: Human, cDNA to mRNA.
FEATURES
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QY 1 GAGCAGGGCCATAATTAT 18
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Db 78 GAGCAGGGCCATAATTAT 61

RESULT 14
LOCUS AC092533 121688 bp DNA linear PRI 15-APR-2005
DEFINITION Homo sapiens BAC clone RP11-57110 from 2, complete sequence.
ACCESSION AC092533 AC027148
VERSION AC092533.1 GI:14718373
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 121688)
REFERENCE Haakenson,W. and Shah,N.
AUTHORS The sequence of Homo sapiens BAC clone RP11-57110
TITLE Unpublished (2001)
JOURNAL 2 (bases 1 to 121688)
REFERENCE Waterston,R.H.
AUTHORS Direct Submission
TITLE Submitted (14-JUL-2001) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 121688)
REFERENCE Waterston,R.H.
AUTHORS Direct Submission
TITLE Submitted (25-JUL-2001) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 121688)
REFERENCE Waterston,R.
AUTHORS Direct Submission
TITLE Submitted (01-MAR-2002) Department of Genetics, Washington
JOURNAL University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 121688)
REFERENCE Wilson,R.K.
AUTHORS Direct Submission
TITLE Submitted (15-APR-2005) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jul 14, 2001 this sequence version replaced gi:7622375.
COMMENT
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
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Center project name: H\_NH0057110  
Drafting Center: WIBR

## NOTICE:

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-125F24, 2000 bp overlap. Actual start of this clone is at base position 9748 of RP11-125F24; actual end is at base position 121688 of RP11-57110.

The sequence of AC027148 has been incorporated into AC092533.

FEATURES  
source

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    complement(82833..82984)
    gene="FSHR"
    note="Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 1, mRNA.; H_NH0057110.1"
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Gaps 0;  
Matches 18; Conservative 0; Indels 0;

Qy 1 GAGCAGGCCCATATTAT 18  
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Db 82973 GAGCAGGCCCATATTAT 82990  
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RESULT 15  
AC083827

LOCUS AC083827 158709 bp DNA linear HTG 24-JAN-2002  
DEFINITION Homo sapiens chromosome 2 clone RP11-345C21, WORKING DRAFT  
SEQUENCE, 23 unordered pieces.  
ACCESSION AC083827  
VERSION AC083827.2 GI:15375221  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 158709)  
AUTHORS Waterston, R.H.  
TITLE The sequence of Homo sapiens clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 158709)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (02-OCT-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
COMMENT On Aug 30, 2001 this sequence version replaced gi:10445290.  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
----- Project Information -----  
Center project name: H\_NH0345C21  
----- Summary Statistics -----  
Sequencing vector: M13, 100%  
Sequencing vector: plasmid, 0%  
Chemistry: Dye-Primer ET; 8% of reads  
Chemistry: Dye-terminator Big Dye, 92% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 142571 bases at least Q40  
Consensus quality: 147681 bases at least Q30  
Consensus quality: 150874 bases at least Q20  
Insert size: 167000; agarose-fp  
Insert size: 156781; sum-of-contigs  
Quality coverage: 3.10 in Q20 bases; agarose-fp  
Quality coverage: 3.36 in Q20 bases; sum-of-contigs  
----- NOTE: This is a 'working draft' sequence. It currently  
\* consists of 23 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 1192: contig of 1192 bp in length  
\* 1193 1292: gap of unknown length  
\* 1293 2772: contig of 1480 bp in length  
\* 2773 2872: gap of unknown length  
\* 2873 4401: contig of 1529 bp in length  
\* 4402 4501: gap of unknown length  
\* 4502 6753: contig of 2252 bp in length  
\* 6754 6853: gap of unknown length  
\* 6854 8763: contig of 1910 bp in length  
\* 8764 8863: gap of unknown length  
\* 8864 11063: contig of 2200 bp in length  
\* 11064 11163: gap of unknown length  
\* 11164 14152: contig of 2989 bp in length  
\* 14153 14252: gap of unknown length  
\* 14253 17321: contig of 3069 bp in length  
\* 17322 17422: gap of unknown length  
\* 17423 19872: contig of 2451 bp in length  
\* 19873 22886: contig of 2914 bp in length  
\* 22887 22986: gap of unknown length



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
536.754 Million cell updates/sec

Title: US-10-018-716B-1  
Perfect score: 18  
Sequence: 1 gagcaggccataattat 18

Scoring table: OLIGO\_NUC  
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Searched: 4996997 seqs, 332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	18	4 AAC90409	Aac90409 Human FSH
C 2	18	100.0	18	4 AAC90408	Aac90408 Human FSH
C 3	18	100.0	1922	11 ADP03559	Adp03559 Human GPC
C 4	18	100.0	2019	10 ADC24202	Adc24202 Human NOV
C 5	18	100.0	2179	2 AAT63181	Aat63181 FSH recep
C 6	18	100.0	2180	2 AAQ29377	Aaq29377 FSHR DNA.
C 7	18	100.0	2222	2 AAQ50013	Aaq50013 FSH recep
C 8	18	100.0	2393	8 ABZ42665	Abz42665 Human fol
C 9	18	100.0	2393	10 ADP25503	Adp25503 Binding d
C 10	18	100.0	2393	10 ACS56611	Acs56611 Human sig
C 11	18	100.0	2393	12 ADI56407	Adi56407 Human pol
C 12	18	100.0	2393	12 ADQ29879	Adq29879 Human GPC
C 13	15	83.3	507	13 ADR26224	Adr26224 Breast ca
C 14	15	83.3	612	6 ABT03390	Abt03390 Ovary cel
C 15	15	83.3	628	6 ABT03391	Abt03391 Ovary cel
C 16	15	83.3	2021	13 ADI19293	Adi19293 Plant cdn
C 17	15	83.3	3659	4 ABL12007	Abli12007 Drosophil
C 18	15	83.3	8253	13 ADR84405	Adr84405 Aspergill
C 19	15	83.3	9140	4 ABL12006	Abli12006 Drosophil

20	15	83.3	76829	14	AEA61117	Aea61117 Human FLJ
C 21	15	83.3	180227	13	ABD33268	Abd33268 Human can
C 22	15	83.3	202251	11	ACN44504	Acn44504 Mouse gen
C 23	14	77.8	400	14	AEB67475	Aeb67475 Rice geno
C 24	14	77.8	574	11	ADT97777	Adt97777 Colon can
C 25	14	77.8	574	11	ADX44259	Adx44259 Human cDN
C 26	14	77.8	810	8	ACA36201	Ac36201 Prokaryot
C 27	14	77.8	900	11	ABD01221	Abd01221 Klebsiell
C 28	14	77.8	975	13	ADT45042	Adt45042 Bacterial
C 29	14	77.8	1059	5	AAH65707	Aah65707 C glutam
C 30	14	77.8	1149	4	AAF67932	Aaf67932 Corynebac
C 31	14	77.8	1200	14	ADZ62987	Adz62987 Murine He
C 32	14	77.8	1254	13	ADS59283	Ads59283 Bacterial
C 33	14	77.8	1506	13	ADS48503	Ads48503 Bacterial
C 34	14	77.8	1617	5	AAQ3640	Aaq3640 DNA encod
C 35	14	77.8	1887	4	AAI58166	Aai58166 Human pol
C 36	14	77.8	1887	5	ADQ98372	Adq98372 DNA encod
C 37	14	77.8	1887	9	ADB48132	Adb48132 Novel hum
C 38	14	77.8	1887	13	ADS47940	Ads47940 Bacterial
C 39	14	77.8	1903	4	AAH17958	Aah17958 Human cDN
C 40	14	77.8	2450	10	ADB68874	Adb68874 C. neoFor
C 41	14	77.8	2975	6	AAD29106	Aad29106 Human MDM
C 42	14	77.8	3678	2	AAQ53996	Aaq53996 Equine he
C 43	14	77.8	3678	2	AAX38299	Aax38299 Equine he
C 44	14	77.8	3762	11	ACH99131	Ach99131 Klebsiell
C 45	14	77.8	4262	2	AAT38484	Aat38484 Rat petri

ALIGNMENTS

RESULT 1  
AAC90409/c  
ID AAC90409 standard; RNA; 18 BP.

AC AAC90409;

DT 19-MAR-2001 (first entry)

XX Human FSH receptor specific antisense oligonucleotide #2.

XX Human; cytostatic; follicle-stimulating hormone receptor; FSHR;

XX fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.

XX Homo sapiens.

XX WO200073416-A1.

XX 07-DEC-2000.

XX 16-MAY-2000; 2000WO-US013488.

XX 28-MAY-1999; 99US-0136489P.

XX 08-OCT-1999; 99US-0158612P.

XX (UYCI-) UNIV CINCINNATI.

XX Labarbera AR, Zhu C, Wang Y;

XX WPI; 2001-091069/10.

XX New composition for regulating fertility, and for chemoprevention and chemotherapy of cancer, comprises an antisense oligonucleotide that is complementary to a nucleotide sequence of a follicle-stimulating hormone receptor.

XX Claim 13; Page 29; 89pp; English.

XX The present invention relates to a composition, which comprises at least one antisense oligonucleotide that is complementary to follicle-stimulating hormone receptor (FSHR) coding sequence. The present sequence is one such oligonucleotide used in the composition. The composition of the present invention can be used for regulating hormones of a host. The

CC composition is also useful for regulating fertility and menstrual cycle.  
CC In addition, the composition is useful as a chemopreventive or  
CC chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver,  
CC ovary, colon, stomach, or especially ovarian cancers), gestational  
CC trophoblastic tumours or testicular germ cell tumours  
XX  
SQ Sequence 18 BP; 4 A; 5 C; 3 G; 0 T; 6 U; 0 Other;  
  
Query Match 100.0%; Score 18; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGCAGGGCCATAATTAT 18  
18 GAGCAGGGCCATAATTAT 1  
Dy  
  
RESULT 2  
AAC90408  
ID AAC90408 standard; DNA; 18 BP.  
XX  
AC AAC90408;  
XX  
DT 19-MAR-2001 (first entry)  
XX  
DE Human FSH receptor specific antisense oligonucleotide #1.  
XX  
KW Human; cytostatic; follicle-stimulating hormone receptor; FSHR;  
KW fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073416-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 16-MAY-2000; 2000WO-US013488.  
XX  
PR 28-MAY-1999; 99US-0136489P.  
PR 08-OCT-1999; 99US-0158612P.  
XX  
PA (UYCI-) UNIV CINCINNATI.  
XX  
PI Labarbera AR, Zhu C, Wang Y;  
XX  
XX WPI; 2001-091069/10.  
DR  
XX  
PT New composition for regulating fertility, and for chemoprevention and  
PT chemotherapy of cancer, comprises an antisense oligonucleotide that is  
PT complementary to a nucleotide sequence of a follicle-stimulating hormone  
PT receptor.  
XX  
PS Claim 13; Page 29; 89pp; English.  
XX  
CC The present invention relates to a composition, which comprises at least  
CC one antisense oligonucleotide that is complementary to follicle-  
CC stimulating hormone receptor (FSHR) coding sequence. The present sequence  
CC is one such oligonucleotide used in the composition. The composition of  
CC the present invention can be used for regulating hormones of a host. The  
CC composition is also useful for regulating fertility and menstrual cycle.  
CC In addition, the composition is useful as a chemopreventive or  
CC chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver,  
CC ovary, colon, stomach, or especially ovarian cancers), gestational  
CC trophoblastic tumours or testicular germ cell tumours  
XX  
SQ Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 18; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGCAGGGCCATAATTAT 18  
18 GAGCAGGGCCATAATTAT 1

Db 1 GAGCAGGGCCATAATTAT 18  
RESULT 3  
ADP03559/c  
ID ADP03559 standard; DNA; 1922 BP.  
XX  
AC ADP03559;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human GPCR follicle stimulating hormone receptor variant "Gene 4" DNA.  
XX  
KW GPCR; G-protein coupled receptor; neuroprotective; nootropic;  
KW tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;  
KW anticonvulsant; antiparkinsonian; cytosstatic; cardiant; hypotensive;  
KW antianginal; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic;  
KW uropathic; antiallergic; cell cycle regulation; neurological;  
KW severe mental retardation; dyskinesia; brain; spinal cord; affective;  
KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;  
KW eating; HIV infection; cancer; metabolic; pituitary;  
KW chromosome identification; gene therapy; human; ds; gene;  
KW follicle stimulating hormone; FSH receptor variant.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 17..1753  
FT /\*tag= a  
FT /product= "Human GPCR follicle stimulating hormone  
FT receptor variant "Gene 4" protein"  
XX  
PN WO20003062393-A2.  
XX  
PD 31-JUL-2003.  
XX  
PF 22-JAN-2003; 2003WO-US001911.  
XX  
PR 22-JAN-2002; 2002US-0350724P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Ramanathan CS, Gopal S, Mintier G, Feder JN;  
XX  
XX WPI; 2003-618283/58.  
DR P-PSDB; ADP03570.  
XX  
PT New nucleic acid molecule encoding a human G-protein coupled receptor,  
PT useful for diagnosing, preventing or treating diseases involving the  
PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or  
PT cancer.  
XX  
PS Claim 1; SEQ ID NO 4; 224pp; English.  
XX  
CC The invention relates to a novel isolated GPCR (G-protein coupled  
CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of  
CC the invention demonstrate neuroprotective, nootropic, tranquiliser,  
CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,  
CC antiparkinsonian, cytosstatic, cardiant, hypotensive, antianginal,  
CC analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic,  
CC antiallergic and anti-HIV properties. The nucleic acid molecule and  
CC polypeptide of the invention may be useful in diagnosing, preventing,  
CC treating or ameliorating a medical condition, such as a disorder related  
CC to aberrant G-protein coupled signalling, a disorder related to aberrant  
CC cell cycle regulation, neurological disorders, severe mental retardation  
CC and dyskinesias, brain disorders, spinal cord disorders, affective  
CC disorders, immune-related disorders, cardiovascular disorders, growth  
CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
CC chromosome identification, in identifying organisms from minute  
CC biological samples, in gene therapy or as a molecular weight marker. The  
CC current sequence is that of a human GPCR (G-protein coupled receptor) DNA

CC which was isolated by the method of the invention.

XX Sequence 1922 BP; 499 A; 504 C; 387 G; 532 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 18; DB 11; Length 1922;  
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0

QY 1 GAGCAGGGCCATAAATTAT 18

Db 28 GAGCAGGGCCATAAATTAT 11

RESULT 4

ADC24202/c

ID ADC24202 standard; cDNA; 2019 BP.

XX ADC24202;

DT 18-DEC-2003 (first entry)

XX Human NOV3a encoding cDNA SEQ ID NO:9.

XX human; NOV3a; cardiac; antiarteriosclerotic; hypotensive; vasotropic;  
KW dermatological; anorectic; immunosuppressive; cytostatic;  
KW antiinfertility; haemostatic; anti-HIV; antiparkinsonian; gene therapy;  
KW neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy;  
KW cardiomyopathy; atherosclerosis; hypertension; congenital heart defect;  
KW pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity;  
KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;  
KW prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma;  
KW fertility; haemophilia; graft versus host disease; AIDS;  
KW bronchial asthma; Crohn's disease; multiple sclerosis;  
KW infectious disease; anorexia; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 61..1962

FT /\*tag= a

FT /product= "NOV3a"

XX WO2003076584-A2.

XX 18-SEP-2003.

XX 06-MAR-2003; 2003WO-US006951.

XX 06-MAR-2002; 2002US-0361974P.

XX 19-MAR-2002; 2002US-0365477P.

XX 22-MAR-2002; 2002US-0366928P.

XX 06-AUG-2002; 2002US-0401661P.

XX 05-MAR-2003; 2003US-00401661.

XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Burgess CE, Edinger SR, Gerlach VL, Ji W, Kekuda R;  
PI Li L, Macdougall JR, Miller CE, Millet I, Patturajan M, Pena CSA;  
PI Rieger DK, Sciore P, Shenoy SG, Smithson G, Spytek KA, Stone DU;  
PI Voss EZ, Zhong M;

DR WPI; 2003-722330/68.

DR P-PSDB; ADC24203.

XX New NOV3 polypeptides and nucleic acids, useful for diagnosing or  
PT treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,  
PT obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or  
PT multiple sclerosis.

XX Claim 20; SEQ ID NO 9; 229pp; English.

XX

CC The present invention describes novel human proteins, designated NOVX  
CC proteins. The NOVX sequences have cardiac, antiarteriosclerotic,  
CC hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,  
CC cytostatic, antiinfertility, haemostatic, anti-HIV, antisthmatic,  
CC antiinflammatory, neuroprotective, anabolic, nootropic and  
CC antiparkinsonian activities, and can be used in gene therapy. The NOVX  
CC sequences can be used as a therapeutic in the manufacture of a medicament  
CC for treating a syndrome associated with a human disease, such as a  
CC pathology associated with NOVX. The NOVX proteins and nucleic acids  
CC encoding them are useful for diagnosing or treating pathologies, diseases  
CC or conditions associated with NOVX sequences, including cardiomyopathy,  
CC atherosclerosis, hypertension, congenital heart defects, pulmonary  
CC stenosis, scleroderma, obesity, metabolic disturbances associated with  
CC obesity, transplantation, adrenoleukodystrophy, congenital adrenal  
CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,  
CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,  
CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious  
CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,  
CC or Parkinson's disease), immune disorders, haematopoietic disorders,  
CC dyslipidaemias, and wasting disorders associated with chronic diseases.  
CC The proteins can also be used as immunogens to produce antibodies and as  
CC vaccines. The sequences may further be used in chromosome mapping,  
CC identifying individual from minute biological samples (tissue typing),  
CC and in forensic identification of a biological sample. The present  
CC sequence encodes human NOV3a from the present invention.

SQ Sequence 2019 BP; 527 A; 514 C; 411 G; 567 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 2019;

Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0

QY 1 GAGCAGGGCCATAAATTAT 18

Db 72 GAGCAGGGCCATAAATTAT 55

RESULT 5

AAT63181/c

ID AAT63181 standard; DNA; 2179 BP.

XX AC AAT63181;

DT 20-JUN-1997 (first entry)

XX FSH receptor gene wild-type allele.

XX Follicle stimulating hormone receptor; FSH receptor; ovarian dysgenesis;  
KW hypergonadotropic hypogonadism; diagnosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT exon 70..227

FT /\*tag= c

FT /note= "nucleotides 70-227 correspond to nucleotides 1-

FT 158 of fshr exon 1"

FT 75..2159

FT /\*tag= a

FT 228..298

FT /\*tag= c

FT /note= "nucleotides 228-298 correspond to nucleotides 7-

FT 77 of fshr exon 2"

FT 299..373

FT /\*tag= c

FT /note= "nucleotides 299-373 correspond to nucleotides 6-

FT 80 of fshr exon 3"

FT 374..450

FT /\*tag= c

FT /note= "nucleotides 374-450 correspond to nucleotides 6-

FT 82 of fshr exon 4"

FT 451..520

FT /\*tag= c

```

FT FT /note= "nucleotides 451-520 correspond to nucleotides 8-
FT exon 521..598
FT /tag= c
FT /note= "nucleotides 521..598 correspond to nucleotides 6-
FT exon 83 of fchr exon 6"
FT 599..668
FT /tag= c
FT /note= "nucleotides 599-668 correspond to nucleotides 6-
FT 75 of fchr exon 7"
FT 640
FT /tag= b
FT /note= "a C to T mutation in codon 189 correlates with
FT ovarian dysgenesis"
FT exon 669..742
FT /tag= c
FT /note= "nucleotides 669-742 correspond to nucleotides 7-
FT 80 of fchr exon 8"
FT 743..928
FT /tag= c
FT /note= "nucleotides 743-928 correspond to nucleotides 6-
FT 191 of fchr exon 9"
FT 929..2179
FT /tag= c
FT /note= "nucleotides 929-2179 correspond to nucleotides
FT 102-1352 of fchr exon 10"
FT
XX WO9711194-A1.
XX
XX 27-MAR-1997.
XX
XX 20-SEP-1996; 96WO-FI000501.
XX
XX 20-SEP-1995; 95US-00531070.
XX
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX De La Chapelle A, Alttomaeki K, Huhtaniemi I;
XX WPI; 1997-202900/18.
XX P-PSDB; AAW14782.
XX
XX Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities - by
XX amplifying DNA including follicle stimulating hormone receptor allele(s),
XX i.e. codon 189, cleaving fragments, and examination.
XX
XX Claim 17; Page 18-21; 43pp; English.
XX
XX A DNA sequence (AAT63181) comprises the coding region from exon 1-10 of
XX the wild-type fchr gene that codes for human follicle stimulating hormone
XX (FSH) receptor (AAW14782). A C to T mutation in exon 7 (codon 189) is
XX associated with ovarian dysgenesis. In a method for determining a FSH
XX receptor genotype in a human patient, fchr exon 7, or a portion of it, is
XX isolated by PCR amplification (see also AAT63195-96) and exposed to BsmI.
XX Exon 7 contains a unique BsmI site which, if mutated, will produce no
XX BsmI digestion products, thereby enabling diagnosis of ovarian dysgenesis
XX
XX Sequence 2179 BP; 575 A; 561 C; 444 G; 599 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 2179;
XX Best Local Similarity 100.0%; Pred. No. 1.3;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAGCAGGGCCCAATATAT 18
XX |||||||||||||||
XX DB 86 GAGCAGGGCCCAATATAT 69
XX
XX RESULT 6
XX AAQ29377/c
XX ID AAQ29377 standard; DNA; 2180 BP.
XX
XX AC AAQ29377;

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XX 25-MAR-2003 (revised)
XX 04-MAR-1993 (first entry)
XX
XX FSHR DNA.
XX
XX Human; follicle stimulating hormone receptor; maturation;
XX spermatogenesis; birth control; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 75..2159
XX /tag= a
XX sig_peptide 75..126
XX /tag= b
XX mat_peptide 127..2159
XX /tag= c
XX
XX WO9216620-A1.
XX
XX 01-OCT-1992.
XX
XX 02-JAN-1992; 92WO-US000122.
XX
XX 15-MAR-1991; 91US-00670085.
XX
XX (ISTF) ARS APPL RES SYST HOLDING NV.
XX
XX Kelton CA, Cheng SVY, Nugent NP, Schweickhardt RL;
XX
XX WPI; 1992-349206/42.
XX P-PSDB; AAR29377.
XX
XX Pure human FSH receptor, fragments and mutants - for preventing follicle
XX growth, maturation and spermatogenesis, also for use of appropriate cell
XX lines for bio-assays of FSH.
XX
XX Claim 7; Page 25; 48pp; English.
XX
XX The DNA sequence encoding human follicle stimulating hormone receptor
XX (FSHR) was obt'd. by screening a lambda gt11 cDNA library constructed from
XX RNA extracted from human testis and amplified, with a rat FSHR cDNA clone
XX as a probe. Positive colonies were used for a secondary screen which
XX isolated five putative human FSHR clones. None of the clones contained
XX the complete hFSHR coding region but could be overlapped using cgc to
XX give the complete sequence. hFSHR binds to FSH to reduce endogenous FSH
XX bioactivity, in females to prevent follicle growth and maturation and in
XX CC males to prevent spermatogenesis, i.e. as a birth control agent. (Updated
XX on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 2180 BP; 577 A; 560 C; 444 G; 599 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 2180;
XX Best Local Similarity 100.0%; Pred. No. 1.3;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAGCAGGGCCCAATATAT 18
XX |||||||||||||||
XX DB 87 GAGCAGGGCCCAATATAT 70
XX
XX RESULT 7
XX AAQ50013/c
XX ID AAQ50013 standard; cDNA to mRNA; 2222 BP.
XX
XX AC AAQ50013;
XX
XX 25-MAR-2003 (revised)
XX 05-MAY-1994 (first entry)
XX
XX FSH receptor.
XX

```



```
KW FSH; receptor; follicle stimulating hormone; GST;
KW glutathione-S-transferase; primer; PCR; amplification;
KW polymerase chain reaction; probe; antibody; overstimulation; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 85..2172
FT     /tag= a
FT     /product= "FSH_receptor"
FT     primer_bind 136..151
FT     /tag= b
FT     /note= "first primer for GST-FSH-R1 and for GST-FSH-R2"
FT     primer_bind 763..776
FT     /tag= d
FT     /note= "primer for GST-FSH-R3"
FT     primer_bind complement(770..787)
FT     /tag= f
FT     /note= "primer for GST-FSH-R2"
FT     primer_bind complement(1167..1183)
FT     /tag= e
FT     /note= "primer for GST-FSH-R1 and for GST-FSH-R3"
FT     primer_bind 1168..1183
FT     /tag= c
FT     /note= "primer for GST-FSH-R3"
XX
PN WO9320199-A1.
XX
PD 14-OCT-1993.
XX
PF 29-MAR-1993; 93WO-EP000780.
XX
PR 30-MAR-1992; 92EP-00200886.
XX
PA (ALKU ) AKZO NV.
XX
PI Dijkema R, De Leeuw R;
XX
WPI: 1993-336907/42.
P-PSDB; AAR42082.
XX
New follicle stimulating hormone receptor - and derived antibodies, anti-
idiotypic antibodies, and transfected cells, useful e.g. in diagnosis and
as antidote for FSH overstimulation.
XX
Disclosure; Page 20-23; 42pp; English.
XX
The primers given in AAO50029-34 were used in the cloning of GST-FSH- R1,
GST-FSH-R2 and GST-FSH-R3 fusion protein constructs. Screening of the
human testis cDNA library with a hFSH-R specific probe resulted in five
recombinant phages positive in hybridisation. Sequence analysis was
performed of the 2222 bp fragment of pGEM3Zc1 (AAQ50013). (Updated on 25-
MAR-2003 to correct FN field.)
XX
Sequence 2222 BP; 598 A; 565 C; 453 G; 606 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 2; Length 2222;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGGGCCATAATTAT 18
DB 96 GAGCAGGGCCATAATTAT 79
RESULT 8
ABZ42665/c
ID ABZ42665 standard; DNA; 2393 BP.
XX
AC ABZ42665;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human follicle stimulating hormone receptor nucleotide SEQ ID NO:121.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP;
XX
WPI: 2003-046718/04.
P-PSDB; ABP81819.
XX
New isolated antigenic peptides e.g., for G protein-coupled receptors
(GPCR), useful for diagnosing and designing drugs for treating conditions
in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
autoimmune diseases.
XX
Disclosure; Fig 1; 523pp; English.
XX
The present invention describes antigenic peptides (I) comprising: (a)
any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
acids. Also described: (1) an assay for the detection of a particular G
protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
and (2) an isolated antibody having high specificity and high affinity or
avidity for a particular GPCR. (I) can be used as GPCR modulators and in
gene therapy. The antigenic peptides for GPCRs are useful in detecting an
antibody against a particular GPCR, and in the production of specific
antibodies. The peptides and antibodies are also useful for detecting the
presence or absence of corresponding GPCRs. The antigenic peptides for
GPCRs and antibodies are useful for diagnosing and designing drugs for
treating immune-related diseases, growth-related diseases, cell
regeneration-related disease, immunological-related cell proliferative
diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
atherosclerosis, bacterial, fungal, protozoan or viral infections,
osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
inflammation, allergies, Crohn's disease, diabetes, graft versus host
disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
anxiety, depression, schizophrenia, dementia, mental retardation, memory
loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
any other disorder in which GPCRs are involved. The antibodies may be
used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
GPCR proteins given in ABP81675 to ABP82018, which are used in the
exemplification of the present invention
XX
Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 8; Length 2393;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGGGCCATAATTAT 18
DB 78 GAGCAGGGCCATAATTAT 61
```

RESULT 9  
 ADD25503/c  
 ID ADD25503 standard; DNA; 2393 BP.  
 XX AC ADD25503;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE Binding domain-immunoglobulin fusion protein-associated DNA #36.  
 XX KW ds; Binding domain; immunoglobulin; fusion protein; cytostatic;  
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
 KW neuroprotective; hinge region; immunoglobulin heavy chain;  
 KW CH2 constant region; CH3 constant region; IgG1;  
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
 XX OS Unidentified.  
 XX PN US2003118592-A1.  
 XX PD 26-JUN-2003.  
 XX PF 25-JUL-2002; 2002US-00207655.  
 XX PR 17-JAN-2001; 2001US-0367358P.  
 PR 17-JAN-2002; 2002US-00053530.  
 PR 03-JUN-2002; 2002US-0385691P.  
 XX PA (GENE-) GENE-CRAFT INC.  
 XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
 XX WPI; 2003-801317/75.  
 XX PT New binding domain-immunoglobulin fusion protein, useful for treating a  
 PT subject having or suspected of having a malignant condition or a B-cell  
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
 XX PS Disclosure; SEQ ID NO 64; 157pp; English.  
 XX OS Unidentified  
 XX SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 10; Length 2393;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCAGGGCCATAATTAT 18  
 Db 78 GAGCAGGGCCATAATTAT 61  
 RESULT 10  
 ACA56611/c  
 ID ACA56611 standard; cDNA; 2393 BP.  
 XX AC ACA56611;  
 XX DT 06-JUN-2003 (first entry)  
 XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1209.  
 XX KW Human; probe; ss; array element; Parkinson's disease;  
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 XX OS Homo sapiens.

XX PN US6500938-B1.  
 XX PD 31-DEC-2002.  
 XX PF 30-JAN-1998; 98US-00016434.  
 XX PR 30-JAN-1998; 98US-00016434.  
 XX PA (INCY-) INCYTE GENOMICS INC.  
 XX PI Au-Young J, Seilhamer JJ;  
 XX WPI; 2003-352189/33.  
 XX PT Combination of polynucleotide probes, useful as array elements in a  
 PT microarray for monitoring the expression of a number of target  
 PT polynucleotides.  
 XX PS Claim 1; SEQ ID NO 1209; 65pp; English.  
 XX CC The invention relates to a combination which, comprises a number of  
 CC polynucleotide probes comprising a sequence selected from one of the 1490  
 CC sequences mentioned in the specification. The combination is useful as an  
 CC array element in a microarray for monitoring the expression of a number  
 CC of target polynucleotides. The microarray is particularly useful in the  
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 CC The microarray is useful in diagnostics and treatment regimens, drug  
 CC discovery and development, toxicological and carcinogenicity studies,  
 CC forensics and pharmacogenomics. The microarray is also useful for  
 CC monitoring progression of diseases and for developing sophisticated  
 CC profiles for the effects of currently available therapeutic drugs. The  
 CC combination is also useful for purifying a subpopulation of mRNAs. CDNAs  
 CC and genomic fragments and in research and diagnostic applications. The  
 CC array can detect changes in expression in a large number of genes coding  
 CC for different signalling pathway populations which can be used to diagnose  
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 CC and Parkinson's disease. The present sequence represents a polynucleotide  
 CC probe of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=06500938B1  
 XX SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 10; Length 2393;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCAGGGCCATAATTAT 18  
 Db 78 GAGCAGGGCCATAATTAT 61  
 RESULT 11  
 ADI56407/c  
 ID ADI56407 standard; DNA; 2393 BP.  
 XX AC ADI56407;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Human polynucleotide probe #1209.  
 XX KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;  
 KW effector-like polypeptide; cancer; immunopathology; neuropathology;  
 KW drug development; toxicology; carcinogenicity;  
 KW signalling pathway polypeptide; adrenal gland; bone;  
 KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
 KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;  
 KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.  
 XX OS

OS Homo sapiens.  
XX US2004010136-A1.  
PN  
XX  
PD 15-JAN-2004.  
XX  
XX 26-NOV-2002; 2002US-00305720.  
PF  
XX 30-JAN-1998; 98US-00016434.  
PR  
XX (INCY- ) INCYTE GENOMICS INC.  
PA  
XX Au-Young J, Seilhamer JJ;  
PI  
XX WPI; 2004-090520/09.  
DR  
XX  
XX New composition comprising polynucleotide probes, useful as array  
PT elements in a microarray for monitoring the expression of target  
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
PT fragments.  
XX  
XX Claim 6; SEQ ID NO 1209; 73pp; English.  
PS  
XX The invention relates to a composition of polynucleotide probes  
CC comprising first polynucleotide probes comprising at least a portion of a  
CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
CC comprising at least a portion of a gene encoding a transducing  
CC polypeptide and third polynucleotide probes comprising at least a portion  
CC of a gene encoding an effector-like polypeptide. The probes of the  
CC composition are useful as array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray is useful in the  
CC diagnosis and treatment of cancer, an immunopathology or a  
CC neuropathology. It can also be used for drug discovery and development,  
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.  
CC Microarrays can also be used for monitoring the progression of diseases  
CC that may be associated with the altered expression of signalling pathway  
CC polypeptides. The composition can also be used to purify a subpopulation  
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of  
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
CC human polynucleotide probe of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
XX Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 18; DB 12; Length 2393;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGGGCCATAATTAT 18  
Db 78 GAGCAGGGCCATAATTAT 61  
RESULT 12  
AD029879/c  
ID AD029879 standard; cDNA; 2393 BP.  
AC AD029879;  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX Human GPCR FSHR polynucleotide, SEQ ID NO:981.  
DE  
XX  
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;

KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
KW gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO2004040000-A2.  
PN  
XX 13-MAY-2004.  
PD  
XX 09-SEP-2003; 2003WO-US028226.  
XX  
PF 09-SEP-2002; 2002US-0409303P.  
PR  
XX 09-APR-2003; 2003US-0461329P.  
PR  
XX (PRIM-) PRIMAL INC.  
PA  
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX  
XX WPI; 2004-390329/36.  
DR P-PSDB; ADO29321.  
XX  
XX Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
XX Claim 151; SEQ ID NO 981; 542pp; English.  
PS  
XX The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridise to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g. Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g. cancers). The present sequence represents a GPCR-encoding  
CC nucleic acid of the invention. Note: The full sequence data for this  
CC patent did not form part of the printed specification; those sequences  
CC not shown were obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 18; DB 12; Length 2393;



PA (DIAD-) DIADEXUS INC.  
XX  
PI Sun Y, Recipon H, Salceda S, Liu C;  
XX  
DR WPI; 2002-519297/55.  
XX  
PT Polypeptide and polynucleotides present in normal and neoplastic ovary  
PT cells, useful for identifying, monitoring, staging, diagnosing,  
PT preventing and treating ovarian cancer, and non-cancerous disease states  
PT in the ovary.  
XX  
PS Claim 1; Page 192-193; 247pp; English.  
XX  
CC The invention comprises amino acid and DNA sequences which are present in  
CC normal and neoplastic ovary cells. The DNA and protein sequences of the  
CC invention are useful for determining the presence of an ovary specific  
CC nucleic acid or an ovary specific protein in a sample. The DNA and  
CC protein sequences of the invention are useful for diagnosing and  
CC monitoring the presence and metastasis of ovarian cancer and breast  
CC cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell  
CC specific DNA sequences of the invention  
XX  
SQ Sequence 628 BP; 202 A; 115 C; 102 G; 209 T; 0 U; 0 Other;  
  
Query Match 83.3%; Score 15; DB 6; Length 628;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AGCAGGGCCCATTAATT 16  
| | | | | | | | | | | | | | | |  
Db 319 AGCAGGGCCCATTAATT 305

Search completed: November 29, 2005, 23:12:28  
Job time : 227.5 secs

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; ORGANISM: Homo sapiens
; TISSUE TYPE: Testis
; IMMEDIATE SOURCE:
; LIBRARY: lgt11 cDNA library, Clontech #HLL1010b
; CLONE: pFHSR11-11, pFHSR15-6
; FEATURE:
; NAME/KEY: protein coding region
; LOCATION: 75 to 2159
US-08-487-886-1

Query Match      100.0%; Score 18; DB 2; Length 2179;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGCAGGGCCATAATTAT 18
Db      |||||
        86 GAGCAGGGCCATAATTAT 69

RESULT 2
US-08-531-070A-1/c
; Sequence 1, Application US/08531070A
; Patent No. 5851768
; GENERAL INFORMATION:
; APPLICANT: de la Chapelle, Albert
; APPLICANT: Aittomaki, Kristiina
; APPLICANT: Huhtaniemi, Ilpo
; TITLE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesisis
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,070A
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/32879
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2179 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-531-070A-1

Query Match      100.0%; Score 18; DB 2; Length 2179;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGCAGGGCCATAATTAT 18
Db      |||||
        86 GAGCAGGGCCATAATTAT 69

RESULT 3
US-08-482-855-1/c
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```
; Sequence 1, Application US/08482855
; Patent No. 6121016
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 6121016een Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; TITLE OF INVENTION: Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESSEE: Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,855
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670,085
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2179
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Testis
; IMMEDIATE SOURCE:
; LIBRARY: lgt11 cDNA library, Clontech #HLL1010b
; CLONE: pFHSR11-11, pFHSR15-6
; FEATURE:
; NAME/KEY: protein coding region
; LOCATION: 75 to 2159
US-08-482-855-1

Query Match      100.0%; Score 18; DB 3; Length 2179;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGCAGGGCCATAATTAT 18
Db      |||||
        86 GAGCAGGGCCATAATTAT 69

RESULT 4
US-08-474-986-1/c
; Sequence 1, Application US/08474986
; Patent No. 6372711
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 6372711een Patrice
```



;/ TITLE OF INVENTION: Human Follicle Stimulating  
;/ HORMONE RECEPTOR  
;/ NUMBER OF SEQUENCES: 2  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Stephan P. Williams,  
;/ Ares-Serono, Inc.  
;/ STREET: Exchange Place, 37th floor  
;/ CITY: Boston  
;/ STATE: MA  
;/ COUNTRY: USA  
;/ ZIP: 02109  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
;/ COMPUTER: IBM PS/2, model 55 SX  
;/ OPERATING SYSTEM: MS-DOS version 4.0  
;/ SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/474,986  
;/ FILING DATE: 07-Jun-1995  
;/ CLASSIFICATION: <Unknown>  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/670,085  
;/ FILING DATE: <Unknown>  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Williams, Stephan P.  
;/ REGISTRATION NUMBER: 28546  
;/ REFERENCE/DOCKET NUMBER: US/252  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (617) 723-1300  
;/ TELEFAX: (617) 723-8923  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 2179  
;/ TYPE: Nucleic acid  
;/ STRANDEDNESS: Double  
;/ TOPOLOGY: Linear  
;/ MOLECULE TYPE: cdna to mRNA  
;/ ORIGINAL SOURCE:  
;/ ORGANISM: Homo sapiens  
;/ TISSUE TYPE: Testis  
;/ IMMEDIATE SOURCE:  
;/ LIBRARY: lgt11 cdna library, Clontech #HL1010b  
;/ CLONE: pFHSR11-11, pFHSR15-6  
;/ FEATURE:  
;/ NAME/KEY: protein coding region  
;/ LOCATION: 75 to 2159  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
;/  
;/ US-08-474-986-1  
;/  
;/ Query Match 100.0%; Score 18; DB 3; Length 2179;  
;/ Best Local Similarity 100.0%; Pred. No. 0.21;  
;/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;/  
;/ QY 1 GAGCAGGGCCATAATTAT 18  
;/ |||||  
;/ Db 86 GAGCAGGGCCATAATTAT 69  
;/  
;/ RESULT 5  
;/ US-09-016-434-1209/c  
;/ Sequence 1209, Application US/09016434  
;/ Patent No. 6500938  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Janice Au-Young  
;/ APPLICANT: Jeffrey J. Sellhamer  
;/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
;/ TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
;/ NUMBER OF SEQUENCES: 1490  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;/ STREET: 3174 PORTER DRIVE  
;/ CITY: PALO ALTO  
;/ STATE: CALIFORNIA

;/ COUNTRY: USA  
;/ ZIP: 94304  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/016,434  
;/ FILING DATE: HEREWITH  
;/ CLASSIFICATION:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER:  
;/ FILING DATE:  
;/ CLASSIFICATION:  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Zeller, Karen J.  
;/ REGISTRATION NUMBER: 37,071  
;/ REFERENCE/DOCKET NUMBER: PA-0002 US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (650) 855-0555  
;/ TELEFAX: (650) 845-4166  
;/ INFORMATION FOR SEQ ID NO: 1209:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 2393 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ IMMEDIATE SOURCE:  
;/ LIBRARY: GENBANK  
;/ CLONE: g182770  
;/ US-09-016-434-1209  
;/  
;/ Query Match 100.0%; Score 18; DB 3; Length 2393;  
;/ Best Local Similarity 100.0%; Pred. No. 0.21;  
;/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;/  
;/ QY 1 GAGCAGGGCCATAATTAT 18  
;/ |||||  
;/ Db 78 GAGCAGGGCCATAATTAT 61  
;/  
;/ RESULT 6  
;/ US-09-270-767-1666/c  
;/ Sequence 1666, Application US/09270767  
;/ Patent No. 6703491  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Homburger et al.  
;/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
;/ FILE REFERENCE: File Reference: 7326-094  
;/ CURRENT APPLICATION NUMBER: US/09/270,767  
;/ CURRENT FILING DATE: 1999-03-17  
;/ NUMBER OF SEQ ID NOS: 62517  
;/ SOFTWARE: PatentIn Ver. 2.0  
;/ SEQ ID NO 1666  
;/ LENGTH: 481  
;/ TYPE: DNA  
;/ ORGANISM: Drosophila melanogaster  
;/ US-09-270-767-1666  
;/  
;/ Query Match 83.3%; Score 15; DB 3; Length 481;  
;/ Best Local Similarity 100.0%; Pred. No. 12;  
;/ Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;/  
;/ QY 1 GAGCAGGGCCATAAT 15  
;/ |||||  
;/ Db 199 GAGCAGGGCCATAAT 185  
;/  
;/ RESULT 7  
;/ US-09-270-767-16948/c  
;/ Sequence 16948, Application US/09270767  
;/ Patent No. 6703491

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16948
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16948

Query Match      83.3%; Score 15; DB 3; Length 481;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGCAGGGCCATAAT 15
        |||||
Db      199 GAGCAGGGCCATAAT 185

RESULT 8
US-09-949-016-16105
; Sequence 16105, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16105
; LENGTH: 52992
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16105

Query Match      83.3%; Score 15; DB 3; Length 52992;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CAGGGCCATAATTAT 18
        |||||
Db      1227 CAGGGCCATAATTAT 1241

RESULT 9
US-09-489-039A-6996/c
; Sequence 6996, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6996
; LENGTH: 900
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; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6996

Query Match      77.8%; Score 14; DB 3; Length 900;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AGCAGGGCCATAAT 15
        |||||
Db      137 AGCAGGGCCATAAT 124

RESULT 10
US-09-602-787A-379/c
; Sequence 379, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schöder, Hartwig
; APPLICANT: Zeider, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
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; ORGANISM: Klebsiella pneumoniae  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1044),(1659)  
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.  
US-09-489-039A-4926

Query Match 77.8%; Score 14; DB 3; Length 3762;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGCAGGCCATAA 14  
|||||  
Db 3709 GAGCAGGCCATAA 3722

RESULT 14  
US-09-949-016-15014/c  
; Sequence 15014, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15014  
; LENGTH: 55264  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15014

Query Match 77.8%; Score 14; DB 3; Length 55264;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CAGGGCCATAATTA 17  
|||||  
Db 41078 CAGGGCCATAATTA 41065

RESULT 15  
US-09-949-016-12122  
; Sequence 12122, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12122  
; LENGTH: 70828  
; TYPE: DNA  
; ORGANISM: Human

; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(70828)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12122  
  
Query Match 77.8%; Score 14; DB 3; Length 70828;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CAGGGCCATAATTA 17  
|||||  
Db 35400 CAGGGCCATAATTA 35413  
  
Search completed: November 29, 2005, 18:24:59  
Job time : 73 secs